

SEARCH REQUEST FORM

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Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

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	Type of Search	Vendors and cost where applicable
Searcher: <u>Jan</u>	NA Sequence (#) _____	STN _____
Searcher Phone #: <u>4498</u>	AA Sequence (#) <input checked="" type="checkbox"/>	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>3/26/03</u>	Bibliographic _____	Dr.Link _____
Date Completed: <u>3/26/03</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/>
Clerical Prep Time: <u>10</u>	Patent Family _____	WWW/Internet _____
Online Time: <u>10</u>	Other _____	Other (specify) _____

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GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 07:31:10 ; Search time 11 seconds
(without alignments)
942.644 Million cell updates/sec

Title: US-09-724-341-8

Perfect score: 1304
Sequence: 1 MPASSPFLAPKGPENMG.....RARKLNLSPHGLFGLVXL 250

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
a1 number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1304	100.0	250	TN13_HUMAN	Q75888 homo sapien
2	1014.5	77.8	241	TN13_MOUSE	Q9d777 mus musculu
3	244.5	18.8	285	T113B_HUMAN	Q9y275 homo sapien
4	234.5	18.0	309	T113B_MOUSE	Q9w472 mus musculu
5	131	10.0	391	EDA_BOVIN	Q9b6g5 bos taurus
6	131	10.0	391	EDA_HUMAN	Q92838 homo sapien
7	131	10.0	391	EDA_MOUSE	Q94653 mus musculu
8	107.5	8.2	234	TNFA_CAVPO	P51435 cavia porce
9	105	8.1	235	TNFA_RAT	P16599 rattus norv
10	104	8.0	233	TNFA_PAPSP	P33620 papio sp. (
11	103.5	7.9	233	TNFA_HUMAN	P01375 homo sapien
12	103	7.9	232	TNFA_CHICK	Q91868 gallus gall
13	102.5	7.9	235	TNFA_RABIT	P04924 corycolagus
14	102.5	7.9	280	TNFA_MACMU	Q9my16 macaca mula
15	100	7.7	229	TNFA_CEREL	P51743 cervus elap
16	99.5	7.6	235	TNFA_MOUSE	P06804 mus musculu
17	99	7.6	233	TNFA_BOVIN	Q06599 bos taurus
18	98.5	7.5	233	TNFA_FELCA	P19101 felis silve
19	98	7.5	233	TNFA_MACFA	P79337 macaca fasc
20	98	7.5	233	TNFA_PAPMU	P48094 macaca mula
21	98	7.5	233	TNFA_PAPHU	Q77510 papio hamad
22	97.5	7.5	233	TNFA_HORSE	P29553 equus cabal
23	97	7.4	280	TNFA_CERTO	Q9bdn1 cercocebus
24	96.5	7.4	291	TN10_MOUSE	P50592 mus musculu
25	95.5	7.3	233	TNFA_CANFA	P51742 canis fami
26	94.5	7.2	235	TNFA_PERLE	P26939 peromyscus
27	93	7.1	233	TNFA_DELE	Q5734 delphinapte
28	93	7.1	233	TNFA_MARMO	C05734 marmota mon
29	93	7.1	281	TNFA_HUMAN	P48023 homo sapien
30	92.5	7.1	233	TNFA_TURTR	Q9bea1 turstopis tr
31	92.5	7.1	278	TNFA_RAT	P56940 rattus norv
32	92	7.1	234	TNFA_SHEEP	P23363 ovis aries
33	91.5	7.0	234	TNFA_CADHI	P13296 capra hircu

ALIGNMENTS

RESULT 1

TN13_HUMAN	STANDARD;	PRT;	250 AA.
AC	Q75888; Q9P1M8; Q9P1M9; Q96HV6;		
DT	15-OCT-2001 (Rel. 40, Created)		
DT	15-OCT-2001 (Rel. 40, Last sequence update)		
DE	Tumor necrosis factor ligand superfamily member 13 (A proliferation-inducing ligand) (APRIL) (TNF- and APO1-related leukocyte expressed ligand 2) (TAL-2) (TNF-related death ligand-1) (TRDL-1).		
GN	TNFRF13 OR APRIL OR TAL2 OR ZTNF2.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_Taxid=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Uterus;		
RX	MEDLINE=98416181; PubMed=9743536;		
RA	Hahne M., Kataoka T., Schroeder M., Hofmann K., Irmeler M., Bodmer J.-L., Schneider P., Bormand T., Holler N., French L.E., Sordet B., Rimoldi D., Tschopp J.;		
RT	"APRIL, a new ligand of the tumor necrosis factor family, stimulates tumor cell growth."		
RL	J. Exp. Med. 188:1185-1190 (1998).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=99260341; PubMed=10331498;		
RA	Shu H.-B., Hu W.-H., Johnson H.;		
RT	"TAL-1 is a novel member of the TNF family that is down-regulated by mitogens."		
RL	J. Leukoc. Biol. 65:680-683 (1999).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RA	Farrar T., Grant F., Haldeman B., Whitmore T., Gross J., O'Hara P.;		
RT	"Homo sapiens tumor necrosis factor homolog."		
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA AND GAMMA).		
RX	MEDLINE=2016836; PubMed=10706119;		
RA	Kelly K.A., Manos E.J., Jensen G.T., Nadalid L., Jones D.A.;		
RT	"APRIL/TRDL-1, a tumor necrosis factor-like ligand, stimulates cell death."		
RL	Cancer Res. 60:1021-1027 (2000).		
RN	[5]		
RP	SEQUENCE OF 1-247 FROM N.A.		
RC	TISSUE=Ovary;		
RA	Strausberg R.;		
RL	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.		
RN	[6]		
RP	FUNCTION.		
RX	MEDLINE=21170294; PubMed=10973284;		
RA	Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M., McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Scollina M., Boyle W.J., Sarsol I., Hsu H., Senaldi G., Theill L.E.;		
RT	"APRIL and TAL-1 and receptors BCMA and TACI: system for regulating		

RT humoral immunity." 170
 RL Nat. Immunol. 1:252-256(2000).
 RN (7)
 RP PROCESSING BY FURIN. MUTAGENESIS OF ARG-101 AND ARG-104, AND
 RX SUBCELLULAR LOCATION.
 RA PubMed=11571266;
 RA Lopez-Fraga M., Fernandez R., Albar J.P., Hahne M.;
 RT "Biologically active APRIL is secreted following intracellular
 processing in the Golgi apparatus by furin convertase.";
 RL EMBO Rep. 2:945-951(2001).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF13B/TACI and to
 CC TNFRSF17/BCMA. May be implicated in the regulation of tumor cell
 CC growth. May be involved in monocyte/macrophage-mediated
 CC immunological processes.
 CC -1- SUBUNIT: Homotrimer (Potential).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC GAMMA; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN TRANSFORMED CELL
 CC LINES. CANCERS OF COLON, THYROID, LYMPHOID TISSUES AND
 CC SPECIFICALLY EXPRESSED IN MONOCYTES AND MACROPHAGES.
 CC -1- INDUCTION: DOWN-REGULATED BY PHORBOL MYRISTATE ACETATE/IONOMYCIN
 CC TREATMENT.
 CC -1- PTM: The precursor is cleaved by furin.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -----
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 DR EMBL: AF046888; AACG1312.1; -
 DR EMBL: AF136294; AAD29422.1; -
 DR EMBL: AF184972; AAF01321.1; -
 DR EMBL: AF114011; AAF59828.1; -
 DR EMBL: AF114012; AAF59829.1; -
 DR EMBL: AF114013; AAF59830.1; -
 DR EMBL: BC008042; AAH08042.1; -
 DR Genbank: HGNC:11928; TNFRSF13.
 DR MIM: 604472; -
 DR InterPro: IPR000478; TNF_family.
 DR Pfam: PF00229; TNF_1.
 DR SMART: SMO0207; TNF_1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 DR Cytokine; Cytotoxin; Immune response; Glycoprotein;
 DR Alternative splicing.
 FT PROPEP 1 104
 FT CHAIN 105 250
 FT SITE 104 105 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 FT DISULFID 196 211 CLEAVAGE (BY FURIN).
 FT CARBOHYD 124 124 POTENTIAL.
 FT VASPPIC 113 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VASPPIC 247 249 KOHSLHLVPINATSKD -> N (IN ISOFORM BETA).
 FT MUTAGEN 101 104 MISSING (IN ISOFORM GAMMA).
 FT MUTAGEN 101 104 RKR->AKRA. ABOLISHES PROTEOLYTIC
 FT PROCESSING.
 FT CONFLICT 96 96 N->S (IN REF. 5).
 FT CONFLICT 247 247 F->L (IN REF. 5).
 SQ SEQUENCE 250 AA; 27433 MM; AELIAGB9457FE238 CRC64;
 Query Match 100.0%; Score 1304; DB 1; Length 250;
 Best Local Similarity 100.0%; Pred. No. 9,4e-108;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPASSPFLAPGPPGNGGPPVRBALSVALWLSGALGAVACAMALLTOOTELQSILRR 60
 DB 1 MPASSPFLAPGPPGNGGPPVRBALSVALWLSGALGAVACAMALLTOOTELQSILRR 60
 QY 61 EVSRLQGTGSPQNGEGYPMOSLPQSSDALEAWNGERSRRKRAVLTKOKQKSHSVLHL 120

DB 61 EVSRLQGTGSPQNGEGYPMOSLPQSSDALEAWNGERSRRKRAVLTKOKQKSHSVLHL 120
 QY 121 VPVATSKDSDVTEVWMPALRRGRGLQAGYGVRIQDAGVYLLYSQVLFQDFTFMQ 180
 DB 121 VPVATSKDSDVTEVWMPALRRGRGLQAGYGVRIQDAGVYLLYSQVLFQDFTFMQ 180
 QY 181 VSRREGGROETLPRCIRSPSPHDPRAVNSCYSGVFLHOGDILSVIIPRAKMLSP 240
 DB 181 VSRREGGROETLPRCIRSPSPHDPRAVNSCYSGVFLHOGDILSVIIPRAKMLSP 240
 QY 241 HGTFLGFVKL 250
 DB 241 HGTFLGFVKL 250
 RESULT 2
 TN13_MOUSE STANDARD; PRT; 241 AA.
 ID TN13_MOUSE
 AC Q9D777; Q9ERP1;
 DT 15-JUN-2002 (Ref. 41, Created)
 DT 15-JUN-2002 (Ref. 41, Last sequence update)
 DT 15-JUN-2002 (Ref. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 13 (A proliferation-
 DE inducing ligand) (APRIL).
 GN TNFRSF13 OR APRIL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21170294; PubMed=10973284;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh Y.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Stanbly F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Orido T., Furuno M., Aono H., Baldarelli R., Barh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein W.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombauts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohetsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF13B/TACI and to
 CC TNFRSF17/BCMA. May be implicated in the regulation of tumor cell
 CC growth. May be involved in monocyte/macrophage-mediated
 CC immunological processes.
 CC -1- SUBUNIT: Homotrimer (Potential).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.


```

RT "structural basis of Bly's receptor recognition.";
RL Nac. Struct. Biol. 9:288-292(2002).
CC -1- FUNCTION: Cytokine that binds to TNFRSF13B/TACI and TNFRSF17/BCMA.
CC TNFSF13/APRIL binds to the same 2 receptors. Together, they form a
CC 2 ligands-2 receptors pathway involved in the stimulation of B-
CC and T-cell function and the regulation of humoral immunity. A
CC third B-cell specific BAFF-receptor (BAFFR/BR3) promotes the
CC survival of mature B-cells and the B-cell response.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -1- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN PERIPHERAL BLOOD
CC LEUKOCYTES AND IS SPECIFICALLY EXPRESSED IN MONOCYTES AND
CC MACROPHAGES. ALSO FOUND IN THE SPLEEN, LYMPH NODE, BONE MARROW, T-
CC CELLS AND DENDRITIC CELLS. A LOWER EXPRESSION SEEN IN PLACENTA,
CC HEART, LUNG, FETAL LIVER, THYMUS, AND PANCREAS.
CC -1- INDUCTION: UPREGULATED BY EXPOSURE TO INTERFERON-GAMMA. DOWN-
CC REGULATED BY PHORBOL MYRISTATE ACETATE/IONOMYCIN TREATMENT.
CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING.
CC -1- PTM: N-glycosylated.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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DR EMBL: AF136293; AAD29421.1; -
DR EMBL: AF116456; AAD25356.1; -
DR EMBL: AF132600; AAD21092.1; -
DR EMBL: AF186114; AAF01432.1; -
DR EMBL: AF134715; AAF60219.1; -
DR EMBL: AB073225; BAB90856.1; -
DR EMBL: BC020674; AAH20674.1; -
DR PDB: 1KXG; 20-MAR-02.
DR PDB: 1KD7; 12-NOV-02.
DR PDB: 1JH5; 08-FEB-02.
DR PDB: HGNC:11929; TNFSF13B.
DR MIM: 603969; -
DR InterPro: IPR000478; TNF_family.
DR SMART: SM00207; TNF_1; FALSE_NEG.
DR PROSITE: PS00251; TNF_1; FALSE_NEG.
DR PROSITE: PS50049; TNF_2; 1.
DR Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor;
DR 3D-structure; Polymorphism.
CHAIN 1 285
FT CHAIN 134 285 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT DOMAIN 1 46 MEMBER 13B, MEMBRANE FORM.
FT TRANSMEM 47 67 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
FT 67 CYTOPLASMIC (POTENTIAL).
FT 67 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT 67 (POTENTIAL).
FT DOMAIN 68 285 EXTRACELLULAR (POTENTIAL).
FT SITE 133 134 CLEAVAGE.
FT DISULFID 232 245 N-LINKED (GLCNAc. . .)
FT CARBOHYD 124 245 A -> T.
FT CARBOHYD 242 242 N-LINKED (GLCNAc. . .) (HIGH MANNOSE).
FT VARIANT 105 105 A -> T.
FT 105 /FTID=VAR 013483.
SO SEQUENCE 285 AA; 31222 MW; 48BD007A838C6867 CRC64;
Query Match 18.8%; Score 244.5; DB 1; Length 285;
Best Local Similarity 29.7%; Pred. No. 2.3e-14;
Matches 70; Conservative 47; Mismatches 90; Indels 29; Gaps 8;
QY 39 LGAVACAAALLT-----QQTLOSLRREVSRLQGTGSPSONGEGYPPNQSLEPQS--SDA 90
Db 54 LALLSCCTTVSVFYVAALQGDLSLRAELQGHAEKLP-A-GAGAPKAGLEADAVTAG 111

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QY 91 LEAME-----NGERSRRRAVLTKOKKHSHVLHVPINNT-SKDSDEVTEWQPA 141
Db 112 LKIFEPAPPEGNSQNSRNKRAVVOGPEETVTDCLQIDSEFTPIQKQSYFFVPLLS 171
QY 142 LRGRGRQAAGYGRIDDAVLLYSQVLFQDYFTFWGVVSE-----GOGROETLFR 195
Db 172 PKRSALAEKKNILVETGYFFLYGVLTDTKYAMGHILQKKHVPFDELSTVTLFR 231
QY 196 CIRSM-P-SHPDRVNSCYSGAVFHLHOGDILSVIIPARAKNLNLSPHGFLGFVKL 250
Db 232 CIQMPETLPN---NCSYSGIAKLEGGDELQALAPRENQISLDGVTFEFGALKL 284
RESULT 4
ID T13B MOUSE STANDARD; PRT; 309 AA.
AC 09MU72;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 13B (B cell-activating
DE factor) (BAFF).
GN TNFSF13B OR BAFF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99288033; PubMed=10359578;
RA Schneider P., Mackay F., Steiner V., Hofmann K., Bodmer J.-L.,
RA Holler N., Ambrose C., Lawton P., Bixler S., Acha-Orbea H.,
RA Valmorri D., Romero P., Werner-Favre C., Zubler R.H., Browning J.L.,
RA Techopp J.;
RT "BAFF, a novel ligand of the tumor necrosis factor family, stimulates
RT B cell growth.";
RL J. Exp. Med. 189:1747-1756(1999).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT SER-79.
RC STRAIN=NZB;
RX PubMed=11862414;
RA Jiang Y., Ohtsui M., Abe M., Li N., Xiu Y., Wen X.S., Shirai T.,
RA Hirose S.;
RT "Polymorphism and chromosomal mapping of the mouse gene for B-cell
RT activating factor belonging to the tumor necrosis factor family
RT (Baff) and association with the autoimmune phenotype.";
RL Immunogenetics 53:810-813(2001).
CC -1- FUNCTION: Cytokine that binds to TNFRSF13B/TACI and TNFRSF17/BCMA.
CC TNFSF13/APRIL binds to the same 2 receptors. Together, they form a
CC 2 ligands-2 receptors pathway involved in the stimulation of B-
CC and T-cell function and the regulation of humoral immunity. A
CC third B-cell specific BAFF-receptor (BAFFR/BR3) promotes the
CC survival of mature B-cells and the B-cell response.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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DR EMBL: AF119383; AAD22475.1; -
DR EMBL: AF352245; AAL83939.1; -
DR MGD; MGI:1344376; Tnf6f13b.
DR InterPro: IPR000478; TNF_family.
DR SMART: SM00207; TNF_1.

```


DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ectodysplasin A (Ectodermal dysplasia protein) (EDA protein).
 GN ED1 OR EDA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM I), AND VARIANTS EDA HIS-61 AND LEU-69.
 RC TISSUE=Sweat gland;
 RX MEDLINE=9631280; PubMed=8696334;
 RA Kere J., Srivastava A.K., Montonen O., Zonana J., Thomas N.S.T.,
 RA Ferguson B.M., Munoz F., Morgan D., Clarke A., Baybayan P.,
 RA Chen E.Y., Ezer S., Saarialho-Kere U., la Chapelle A.,
 RA Schlessinger D.;
 RT "X-linked anhidrotic (hypohidrotic) ectodermal dysplasia is caused by
 RT mutation in a novel transmembrane protein.";
 RL Nat. Genet. 13:409-416(1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM A1), AND VARIANTS EDA.
 RC TISSUE=Liver;
 RX MEDLINE=98349961; PubMed=9683615;
 RA Montreal A.W., Zonana J., Ferguson B.M.;
 RT "Identification of a new splice form of the ED1 gene permits
 RT detection of nearly all X-linked hypohidrotic ectodermal dysplasia
 RT mutations.";
 RL Am. J. Hum. Genet. 63:380-389(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS A1; A2; B; C; D; E AND F), AND VARIANTS
 RP EDA.
 RX MEDLINE=98409495; PubMed=9736768;
 RA Bayes M., Hartung A.J., Ezer S., Piapa J., Theeleff I.,
 RA Srivastava A.K., Kere J.;
 RT "The anhidrotic ectodermal dysplasia gene (EDA) undergoes alternative
 RT splicing and encodes ectodysplasin-A with deletion mutations in
 RT collagenous repeats.";
 RL Hum. Mol. Genet. 7:1661-1669(1998).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORMS A1 AND C).
 RA Clark S.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP TISSUE SPECIFICITY, AND ALTERNATIVE SPLICING.
 RA Kobielski K., Kobielski A., Trzciak W.H.;
 RT "Expression of a novel transcript isoform of the EDA gene in human
 RT umbilical cord.";
 RL Eur. J. Hum. Genet. Suppl. 7:104-104(1999).
 RN [6]
 RP RECEPTOR INTERACTION (ISOFORMS A1 AND A2).
 RX MEDLINE=20495245; PubMed=1103935;
 RA Yan M., Wang L.-C., Hymowitz S.G., Schilbach S., Lee J., Goddard A.,
 RA de Vos A.M., Gao W.-Q., Dixit V.M.;
 RT "Two-amino acid molecular switch in an epithelial morphogen that
 RT regulates binding to two distinct receptors.";
 RL Science 290:523-527(2000).
 RN [7]
 RP PROCESSING, MUTAGENESIS OF ARG-153, AND CHARACTERIZATION OF VARIANT
 RP H-156.
 RX PubMed=11309369;
 RA Elomaa O., Pulkkinen K., Hannelius U., Mikkola M., Saarialho-Kere U.,
 RA Kere J.;
 RT "Ectodysplasin is released by proteolytic shedding and binds to the
 RT EDAR protein.";
 RL Hum. Mol. Genet. 10:953-962(2001).
 RN [8]
 RP CHARACTERIZATION OF VARIANTS C-155; C-156 AND H-156, MUTAGENESIS OF
 RP ARG-153; ARG-158 AND ARG-159, AND CLEAVAGE SITE.
 RX PubMed=11416205;
 RA Chen Y., Molloy S.S., Thomas L., Gambee J., Baechinger H.P.,
 RA Ferguson B.M., Zonana J., Thomas G., Morris N.P.;
 RT "Mutations within a furin consensus sequence block proteolytic release

RT of ectodysplasin-A and cause X-linked hypohidrotic ectodermal
 RT dysplasia.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7218-7223(2001).
 RN [9]
 RP VARIANT EDA TYR-54.
 RX MEDLINE=98292028; PubMed=9630076;
 RA Hertz J.W., Noergaard Hansen K., Juncker I., Kjeldsen M.,
 RA Gregersen N.;
 RT "A novel missense mutation (402C->T) in exon 1 in the EDA gene in a
 RT family with X-linked hypohidrotic ectodermal dysplasia.";
 RL Clin. Genet. 53:205-209(1998).
 RN [10]
 RP VARIANT EDA LYS-63.
 RX MEDLINE=98188231; PubMed=9507389;
 RA Ferguson B.M., Thomas N.S.T., Munoz F., Morgan D., Clarke A.,
 RA Zonana J.;
 RT "Scarcity of mutations detected in families with X linked hypohidrotic
 RT ectodermal dysplasia: diagnostic implications.";
 RL J. Med. Genet. 35:112-115(1998).
 RN [11]
 RP VARIANT EDA ARG-55.
 RX MEDLINE=9939307; PubMed=10469321;
 RA Martinez F., Millan J.M., Orellana C., Prieto F.;
 RT "X-linked anhidrotic (hypohidrotic) ectodermal dysplasia caused by a
 RT novel mutation in ED1 gene: 406T > G (Leu55Arg).";
 RL J. Invest. Dermatol. 113:285-286(1999).
 RN [12]
 RP VARIANTS EDA R-60; Y-252; V-269; S-302 AND M-378.
 RX PubMed=11378824;
 RA Vincent M.C., Biancalana V., Gintsev D., Mandel J.L., Calvas P.;
 RT "Mutational spectrum of the ED1 gene in X-linked hypohidrotic
 RT ectodermal dysplasia.";
 RL Eur. J. Hum. Genet. 9:355-363(2001).
 RN [13]
 RP VARIANTS EDA C-156; H-156; C-255; D-255; G-274; Y-332 AND T-349.
 RX MEDLINE=21193173; PubMed=11295832;
 RA Peasekkoenen K., Cambiagh S., Novelli G., Ouzts L.V., Penttinen M.,
 RA Kere J., Srivastava A.K.;
 RT "The mutation spectrum of the EDA gene in X-linked anhidrotic
 RT ectodermal dysplasia.";
 RL Hum. Mutat. 17:349-349(2001).
 CC -1- FUNCTION: Seems to be involved in epithelial-mesenchymal signaling
 CC during morphogenesis of ectodermal organs. Isoform A1 binds only
 CC to the receptor EDAR, while isoform A2 binds exclusively to the
 CC receptor XEDAR.
 CC -1- SUBUNIT: Homotrimer.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted.
 CC -1- ALTERNATIVE PRODUCTS: At least 8 isoforms, I, A1/II (shown here),
 CC A2, B, C, D, E and F, are produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: NOT ABUNDANT; EXPRESSED IN SPECIFIC CELL TYPES
 CC OF ECTODERMAL (BUT NOT MESODERMAL) ORIGIN OF KERATINOCYTES, HAIR
 CC FOLLICLES, SWEAT GLANDS. ALSO IN ADULT HEART, LIVER, MUSCLE,
 CC PANCREAS, PROSTATE, PETAL LIVER, UTERUS, SMALL INTESTINE AND
 CC UMBILICAL CHORD.
 CC -1- PTM: N-glycosylated.
 CC -1- DISEASE: DEFECTS IN ED1 ARE THE CAUSE OF X-LINKED ANHIDROTIC
 CC (HYPOHIDROTIC) ECTODERMAL DYSPLASIA (XLEDH OR EDA); A DISEASE
 CC CHARACTERIZED BY SPARSE HAIR (ATRICHOSIS OR HYPOTRICHOSIS),
 CC ABNORMAL OR MISSING GLANDS. EDA IS THE MOST COMMON FORM OF OVER 150
 CC CLINICALLY DISTINCT ECTODERMAL DYSPLASIAS. THIS DISEASE WAS
 CC ALREADY DESCRIBED BY DARWIN.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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[illegible]

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Oy      241 HGTFPGPVKL 250
          |||::||
Db      376 HTTPGAIRL 385

RESULT 7
EDNA_MOUSE
ID_ID_EDA_MOUSE STANDARD; PRT: 391 AA.
AC OS4693; Q35705; Q9QZ01; Q9QMJ8;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ectodysplasin A (EDA protein homolog) (Tabby protein).
GN EDI OR EDA OR TA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
[1]
RN SEQUENCE FROM N.A. (ISOFORMS TAA, TAB AND TAC).
RP STRAIN=129/Sv;
RX MEDLINE=98058770; PubMed=9371801;
RA Srivastava A.K., Pispa J., Hartung A.J., Du Y., Ezer S., Jenks T.,
RA Shimada T., Pekkanen M., Mikkola M.L., Ko M.S.H., Theisloff I.,
RA Kere U., Schlesinger D.;
RT "The Tabby phenotype is caused by mutation in a mouse homologue of the
RT EDA gene that reveals novel mouse and human exons and encodes a
RT protein (ectodysplasin-A) with collagenous domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:13069-13074(1997).
[2]
RN SEQUENCE FROM N.A. (ISOFORM TAD).
RP MEDLINE=97449184; PubMed=9285798;
RA Ferguson B.M., Brockdorff N., Formstone E., Nguyen T.,
RA Kronmiller J.E., Zonana J.;
RT "Cloning of Tabby, the murine homology of the human EDA gene: evidence
RT for a membrane-associated protein with a short collagenous domain.";
RL Hum. Mol. Genet. 6:1589-1594(1997).
[3]
RN SEQUENCE FROM N.A. (ISOFORMS TA-A2 AND TA-A3).
RP TISSUE=Embryo;
RC MEDLINE=20005791; PubMed=10534613;
RX Mikkola M.L., Pispa J., Pekkanen M., Paulin L., Nieminen P., Kere J.,
RA Theisloff I.;
RT "Ectodysplasin, a protein required for epithelial morphogenesis, is a
RT novel TNF homologue and promotes cell-matrix adhesion.";
RL Mech. Dev. 88:133-146(1999).
-1- FUNCTION: Involved in epithelial-mesenchymal signaling during
morphogenesis of ectodermal organs. Isoform TPA binds only to the
receptor EDAR, while isoform TA-A2 binds exclusively to the
receptor XEDAR.
-1- SUBUNIT: Homotrimer (By similarity).
-1- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
similarity).
-1- ALTERNATIVE PRODUCTS: At least 6 isoforms; TAA/A1 (shown here),
TPA-A2, TA-A3, TAB, TAC and TAD; are produced by alternative
splicing.
-1- PTM: N-glycosylated (By similarity).
-1- PTM: Processing by furin produces a secreted form (By similarity).
-1- DISEASE: Defects in EDI are the cause of the tabby phenotype in
humans (the equivalent of anhidrotic ectodermal dysplasia in
mice). The disease is characterized by sparse hair (arichosis
or hypotrichosis), abnormal or missing teeth and the inability to
sweat due to the absence of sweat glands.
-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
-----
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DR EMBL: AF016627; AAB95202.1; -
DR EMBL: AF016628; AAB95203.1; -
DR EMBL: AF016629; AAB95204.1; -
DR EMBL: AF016630; AAB95205.1; -
DR EMBL: AF016631; AAB95206.1; -
DR EMBL: AF004434; AAB88121.1; -
DR EMBL: AF004435; AAB88122.1; -
DR EMBL: Y13438; CA73849.1; -
DR EMBL: AJ243657; CAB52696.1; -
DR EMBL: AJ243658; CAB52697.1; -
DR MCD; MGT1195272; Eda.
DR InterPro; IPR000087; Collagen.
DR Pfam; PF01391; Collagen; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; FALSE_NEG.
DR PROSITE; PS50049; TNF_2; 1.
KW Developmental protein; Differentiation; Transmembrane;
KW Signal-anchor; Glycoprotein; Alternative splicing.
FT CHAIN 1 391
  ECTODYSPLASIN A, SECRETED FORM (BY
  SIMILARITY).
  CYTOPLASMIC (POTENTIAL).
  SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
  (POTENTIAL).
  EXTRACELLULAR (POTENTIAL).
  COLLAGEN-LIKE.
  CLEAVAGE (BY FURIN) (BY SIMILARITY).
  N-LINKED (GLCNAC...) (POTENTIAL).
  MALINFEFPEKAYSEESRRKRSKSGEGADGVK
  KKGKAPGPGPGPGPGPGPGPGPGPGPGPGPG
  GPSPARGLAGAGTLPLRAKFGGRWENAGVGRCPG
  VVLCGCGSRSPSPVSKAPARAPEWMA (IN
  ISOFORM TAC).
  PVKKKKKK -> KSTGVIFEP (IN ISOFORM TAB).
  MISSING (IN ISOFORM TAB).
  MISSING (IN ISOFORM TAC).
  MISSING (IN ISOFORM TA-A3).
  MISSING (IN ISOFORM TAD).
  MISSING (IN ISOFORM TA-A2 AND ISOFORM TA-
  A3).
  D -> E (IN REF. 2).
FT CONFLICT 126 126
FT SEQUENCE 391 AA; 41603 MW; 41603 DEFF; CRC64;
Query Match 10.0%; Score 131; DB 1; Length 391;
Best Local Similarity 23.28; Pred. No. 0.00035;
Matches 58; Conservative 34; Mismatches 100; Indels 58; Gaps 9;
11 PKGPGNGG--GVREPALVALWLSGALGAVACAMALLTQOTELSLREVSRLOGT 68
184 PNGPPGPPGPGPGPGPGPGPGPGPGPGPGPGPGPGPGPGPGPGPGPGPGPG 219
69 GGPSONGSGYWSLPEQSSDALEWENGERSRKRRAVLTKQKKHSHLVLPINAT- 126
220 PGP--PGPGPGPGPGPGPGPGPGPGPGPGPGPGPGPGPGPGPGPGPGPGPG 261
127 SKD-----SDVTEVMQPALRRRGQAGQGYRVIDAGVYLLYSQVLTQDVFTMGQ 180
262 VKNDLSGGVLDWSRTITNPFVK--LHPSGSELEVLDGTYFYSGVEVYINFT--D 316
181 VSRREGQGRQRTFLFRCSRSMSPHPRAYNSCYSAGVFPHQODLSVILPPARAKLNSP 240
317 FASVEVVDKRFLOCTHSIETGKTN-VNTCTYAGVCLLKAKRQKAVACVMAHADISINMSK 375
DB 241 HGTFLGFLVL 250
376 HTFFGAIRL 385
RESULT 8
TNFA_CAVPO STANDARD; PRT; 234 AA.
ID TNFA_CAVPO

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AC P51435;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley; TISSUE=Lung;
RA White A.M., Yoshimura T., Smith A.W., Westwick J., Watson M.L.;
RT "Airway inflammation induced by recombinant guinea pig tumor necrosis
RT factor-alpha". 273:L524-L530(1997).
RL Am. J. Physiol.
CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR2. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia, under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -1- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -1- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC -----
DR EMBL: U39839; AAB06492.1; -
DR EMBL: U77036; AAB19210.1; -
DR HSSP; P06804; 2TNF.
DR InterPro; IPR003636; TNF_abc.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_abc; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Cytotoxin; Transmembrane; Phosphorylation; Signal-anchor.
FT CHAIN 1 234
FT DOMAIN 80 234
FT CHAIN 1 35
FT DOMAIN 1 35
FT TRANSMEM 36 56
FT DOMAIN 57 234
FT SITE 79 80
FT MOD_RES 2 2
  EXTRACELLULAR (POTENTIAL).
  CLEAVAGE (BY ADAM17) (BY SIMILARITY).
  PHOSPHORYLATION (BY CK1) (BY SIMILARITY).

```

FT DISUFID 147 178 BY SIMILARITY
 SO SEQUENCE 234 AA; 25793 MW; 7272C940393E7B9B CRC64;
 Query Match 8.2%; Score 107.5; DB 1; Length 234;
 Best Local Similarity 27.1%; Pred. No. 0.021;
 Matches 49; Conservative 22; Mismatches 61; Indels 49; Gaps 10;
 QY 92 EAMNGERSRRRAVLTKQKKQHS---VHLVPINATSDSDVTEVMQPALRRGRG 147
 DB 62 EQFSSGPEFRPLAQTLLRSASQNDNDRPVHVV-ANQAAEE---ELQW--LSKRANA 113
 QY 148 LQAGGYGR-----IQDAGVLLYSQVDFQDVTFTMGQ-----VSRREGGQRET 192
 DB 114 LLANGMGLSDNQLVPSDGLYISQVLFK-----GGGCSYLLLTHTVSRLLAVSYPEK 167
 QY 193 L-----FRCIRSMPSHPDRA--YNSCYSAGVFHLHOGDILSVIIPRAKLNLSPHGT 243
 DB 168 VNLISAIKSPCKERTBEAERKRPWEPYLYLGSGVQLQKGNLH-----AEVNLPGYLD 220
 244 F 244
 221 F 221
 RESULT 9
 ID TNFA RAT STANDARD; PRT; 235 AA.
 AC P16599;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
 DE 1194 superfamily member 2) (Cachectin).
 GN TNF OR TNFSF2 OR TNFA.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP STRAIN=Sprague-Dawley; TISSUE=Testis;
 RC MEDLINE=9404766; PubMed=8224868;
 RA Kwon J., Chung I.Y., Benveniste E.N.;
 RT "Cloning and sequence analysis of the rat tumor necrosis
 RT factor-encoding genes.";
 RL Gene 132:227-236(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC Shirai T., Shimizu N., Horiguchi S., Ito H.;
 RT "Cloning and expression in Escherichia coli of the gene for rat tumor
 RT necrosis factor.";
 RL Agric. Biol. Chem. 53:1733-1736(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=9232907; PubMed=1627266;
 RA Bedler H.C., Grewe M., Gauselning R., Pavlovic M., Decker K.;
 RT "Rat tumor necrosis factor-alpha. Transcription in rat Kupffer cells
 RT and in vitro posttranslational processing based on a PCR-derived
 RT cDNA.";
 RL Biol. Chem. Hoppe-Seyler 373:271-281(1992).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Various;
 RX MEDLINE=21369712; PubMed=11477479;
 RA Furuya T., Joe B., Saitono J.L., Hashiramoto A., Dobbins D.E.,
 RT "Polymorphisms of the tumor necrosis factor alpha locus among
 RT autoimmune disease susceptible and resistant inbred rat strains.";
 RL Genes Immun. 2:229-232(2001).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Decker K.F.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.

RN [6]
 RP SEQUENCE OF 1-231 FROM N.A.
 RC TISSUE=Tail;
 RA Kiristides M.J., Vardimon D., Kunz H.W., Gill T.J. III;
 RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
 CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
 CC induce cell death of certain tumor cell lines. It is potent
 CC pyrogen causing fever by direct action or by stimulation of
 CC interleukin 1 secretion and is implicated in the induction of
 CC cachexia. Under certain conditions it can stimulate cell
 CC proliferation and induce cell differentiation.
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
 CC extracellular soluble form (By similarity).
 CC -1- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -1- PTM: The membrane form, but not the soluble form, is
 CC phosphorylated on serine residues. Dephosphorylation of the
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
 CC similarity).
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
 CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
 CC AND MALNUTRITION.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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 DR EMBL: X66539; CAA47146.1; -;
 DR EMBL: L00981; AAA16275.1; -;
 DR EMBL: D00475; BAA00367.1; -;
 DR EMBL: AJ002478; CAA05290.1; -;
 DR EMBL: L19123; AAA42255.1; -;
 DR EMBL: AF329982; AAK53568.1; -;
 DR EMBL: AF329983; AAK53569.1; -;
 DR EMBL: AF329984; AAK53570.1; -;
 DR EMBL: AF329985; AAK53571.1; -;
 DR EMBL: AF329986; AAK53572.1; -;
 DR EMBL: AF329987; AAK53573.1; -;
 DR PIR: J00029; J00029.
 DR PIR: S21674; S21674.
 DR PIR: J00868; J00868.
 DR HSSP: P06804; 2TNF.
 DR InterPro: IPR000478; TNF_family.
 DR Pfam: PF00229; TNF_1.
 DR PRINTS: PR01234; TNFCROSISFCT.
 DR ProDom: PD002012; TNF_abc; 1.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 KW Cytokine; Cyclooxygenase; Glycoprotein; Phosphorylation;
 KW Signal-anchor.
 KM
 FT CHAIN 1 235
 FT DOMAIN 80 235
 FT TRANSMEM 1 35
 FT TRANSMEM 36 56
 FT
 FT DOMAIN 57 235
 FT SITE 79 80
 FT MOD_RES 2 2
 FT DISUFID 148 179
 FT CARBOHYD 86 86
 FT CONFLICT 39 39
 FT CONFLICT 163 163
 FT CONFLICT 202 202
 SO SEQUENCE 235 AA; 25806 MW; B808EC6D049C2F3B CRC64;

RT "cloning and expression in Escherichia coli of the gene for human
 RT tumour necrosis factor.";
 RL Nature 313:803-806(1985).
 RN [14]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86016093; PubMed=2995927;
 RA Nedwin G.E., Naylor S.L., Sakaguchi A.Y., Smith D.H.,
 RA Urelett-Nedwin J., Pennica D., Goeddel D.V., Gray P.W.;
 RT "Human lymphotoxin and tumor necrosis factor genes: structure,
 RT homology and chromosomal localization.";
 RL Nucleic Acids Res. 13:6361-6373(1985).
 RN [15]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85142190; PubMed=3856324;
 RA Wang A.M., Creasey A.A., Lachner M.B., Lin L.S., Strickler J.,
 RA van Arsdell J.N., Yamamoto R., Mark D.F.;
 RT "Molecular cloning of the complementary DNA for human tumor necrosis
 RT factor.";
 RL Science 228:149-154(1985).
 RN [16]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86030296; PubMed=3932069;
 RA Marmenout A., Franssen L., Tavernier J., van der Heyden J., Tizard R.,
 RA Kwaesehaert E., Shaw A., Johnson M.J., Semon D., Mueller R.,
 RA Kuysschaert M.R., Van Vliet A., Fiers W.;
 RT "Molecular cloning and expression of human tumor necrosis factor and
 RT comparison with mouse tumor necrosis factor.";
 RL Eur. J. Biochem. 152:515-522(1985).
 RN [17]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93272029; PubMed=8499947;
 RA Itlis F.J.M., Bouguetieret L., Prieux S., Caterina D., Primas G.,
 RA Perrot V., Jurka J., Rodriguez-Tome P., Claverie J.-M., Dausset J.,
 RA Cohen D.;
 RT "Genee Aliu clustering and a potential new member of the NF kappa B
 RT family within a 90 kilobase HLA class III segment.";
 RL Nat. Genet. 3:137-145(1993).
 RN [18]
 RP SEQUENCE FROM N.A.
 RA Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,
 RA Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,
 RA Laaky S., Hood L.;
 RT "Sequence of the human major histocompatibility complex class III
 RT region.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [19]
 RP SEQUENCE FROM N.A.
 RX Shima S., Tamiya G., Oka A., Inoko H.;
 RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP SEQUENCE FROM N.A.
 RX Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
 RA Nickerson D.A.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RN [11]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [12]
 RP PHOSPHORYLATION (MEMBRANE FORM).
 RX PubMed=8597870;
 RA Pocisk E., Duda E., Wallach D.;
 RT "Phosphorylation of the 26 kDa TNF precursor in monocytic cells and in
 RT transfectected HeLa cells.";
 RL J. Inflamm. 45:152-160(1995).
 RN [13]
 RP PHOSPHORYLATION BY CK1, AND DEPHOSPHORYLATION.
 RX PubMed=10205166;
 RA Motte A.D., Hunt N.H., Manigasekara Y., Bloomfield G., Wallach D.,
 RA Roufogalis B.D., Chaudhuri G.;
 RT "A casein kinase I motif present in the cytoplasmic domain of members

RT of the tumour necrosis factor ligand family is implicated in 'reverse
 RT signaling'.";
 RL EMBO J. 18:2119-2126(1999).
 RN [14]
 RP MUTAGENESIS.
 RX MEDLINE=91184128; PubMed=2009860;
 RA Ostadé X.V., Tavernier J., Prange T., Fiers W.;
 RT "Localization of the active site of human tumour necrosis factor
 RT (hTNF) by mutational analysis.";
 RL EMBO J. 10:827-836(1991).
 RN [15]
 RP MYRISTOYLATION
 RX MEDLINE=93018820; PubMed=1402651;
 RA Stevenson F.T., Bursten S.L., Lockley R.M., Lovett D.H.;
 RT "Myristyl acylation of the tumor necrosis factor alpha precursor on
 RT specific lysine residues.";
 RL J. Exp. Med. 176:1053-1062(1992).
 RN [16]
 RP CLEAVAGE BY ADAM17.
 RX MEDLINE=97186575; PubMed=9034191;
 RA Mos M.L., Jin S.-L.C., Milla M.E., Burkhardt W., Carter H.L.,
 RA Chen W.-J., Clay W.C., Didsbury J.R., Haegler D., Hoffman C.R.,
 RA Kost T.A., Lambert M.H., Leesnitzer M.A., McCauley P., McGehee G.,
 RA Mitchell J., Moyer M., Patel G., Rocque W., Overton L.K., Schoenen F.,
 RA Seaton T., Su J.-L., Warner J., Willard D., Becherer J.D.;
 RT "Cloning of a disintegrin metalloproteinase that processes precursor
 RT tumour-necrosis factor-alpha.";
 RL Nature 385:733-736(1997).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=89159409; PubMed=2922050;
 RA Jones E.Y., Stuart D.I., Walker N.P.;
 RT "Structure of tumour necrosis factor.";
 RL Nature 338:225-228(1989).
 RN [18]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=91193276; PubMed=1964681;
 RA Jones E.Y., Stuart D.I., Walker N.P.;
 RT "The structure of tumour necrosis factor -- implications for
 RT biological function.";
 RL J. Cell Sci. Suppl. 13:11-18(1990).
 RN [19]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
 RX MEDLINE=90089932; PubMed=2551905;
 RA Beck M.J., Sprang S.R.;
 RT "The structure of tumor necrosis factor-alpha at 2.6-A resolution.
 RT Implications for receptor binding.";
 RL J. Biol. Chem. 264:17595-17605(1989).
 RN [20]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MUTANT ARG-107.
 RX MEDLINE=98147459; PubMed=9488135;
 RA Reed C., Fu Z.Q., Wu J., Xue Y.N., Harrison R.W., Chen M.J.,
 RA Weber I.T.;
 RT "Crystal structure of TNF-alpha mutant R10D with greater affinity for
 RT receptor R1 compared with R2.";
 RL Protein Eng. 10:1101-1107(1997).
 RN [21]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF MUTANT M3S.
 RX MEDLINE=98113178; PubMed=9442056;
 RA Cha S.S., Kim J.S., Cho H.S., Shin N.K., Jeong W., Shin H.C.,
 RA Kim Y.J., Hahn J.H., Oh B.H.;
 RT "High resolution crystal structure of a human tumor necrosis factor-
 RT alpha mutant with low systemic toxicity.";
 RL J. Biol. Chem. 273:2153-2160(1998).
 RN [22]
 RP FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
 TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
 CC induce cell death of certain tumor cell lines. It is potent
 CC pyrogen causing fever by direct action or by stimulation of
 CC interleukin 1 secretion and is implicated in the induction of
 CC cachexia. Under certain conditions it can stimulate cell
 CC proliferation and induce cell differentiation.
 CC -I- SUBUNIT: Homotrimer.
 CC -I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN

RX	MEDLINE=86219712; PubMed=3519138.
RA	Ito H., Shirai T., Yamamoto S., Akira M., Kawahara S., Todd C.W.,
RT	"Molecular cloning of the gene encoding rabbit tumor necrosis
CC	factor.";
RL	DNA 5:157-165(1986).
RP	[3]
SEQUENCE FROM N.A.	
RX	MEDLINE=86219711; Pubmed=3519137;
RA	Ito H., Yamamoto S., Kuroda S., Sakamoto H., Kajihara J., Kiyoata T.,
RA	Hayaishi H., Kato M., Seko M.;
RT	"Molecular cloning and expression in Escherichia coli of the cDNA
RT	coding for rabbit tumor necrosis factor.";
RT	DNA 5:149-156(1986).
-I-	FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC	TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC	induce cell death of certain tumor cell lines. It is potent
CC	pyrogen causing fever by direct action or by stimulation of
CC	interleukin 1 secretion and is implicated in the induction of
CC	cachexia. Under certain conditions it can stimulate cell
CC	proliferation and induce cell differentiation.
-I-	SUBUNIT: Homotrimer (By similarity).
-I-	SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC	extracellular soluble form (by similarity).
-I-	Ptm: The soluble form derives from the membrane form by
CC	proteolytic processing (By similarity).
-I-	Ptm: The membrane form, but not the soluble form, is
CC	phosphorylated on serine residues. Dephosphorylation of the
CC	membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC	similarity).
CC	-I- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC	CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC	AND MALNUTRITION.
-I-	SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC	-----
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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; M12845; AAAJ1486.1; .
DR	EMBL; M12846; AAAJ1482.1; .
DR	EMBL; M60340; AAAJ1484.1; .
PIR; A25451; A25451.	
PIR; A25454; A25454.	
PIR; JS0727; JS0727.	
HSSP; P06804; 2TNF.	
InterPro; IPRO03636; TNF_abc.	
InterPro; IPRO00478; TNF_family.	
Pfam; PF00229; TNF.1.	
PRINTS; PR01234; TNECROSISFCT.	
Frodem; PD002012; TNF_abc; 1.	
SMART; SM00207; TNF.1.	
PROSITE; PS00251; TNF_1; 1.	
PROSITE; PSS0049; TNF_2; 1.	
KW Cytokine; Cytotoxicity; Transmembrane; Phosphorylation; Signal-anchor.	
CHAIN 1 235	
FT CHAIN 80 235	
FT DOMAIN 1 35	
FT TRANSMEM 36 56	
DOMAIN 57 235	EXTRACELLULAR (POTENTIAL).
SITE 79 80	CLEAVAGE (BY ADAM17) (BY SIMILARITY).
MOD RES 2 2	PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
DISULFID 148 179	BY SIMILARITY.
CONFLICT 63 63	MISSING (IN REF. 3).
SO SEQUENCE 235 AA; 25816 MW; 610177DD0BD2EF871 CRC64;	
Query Match	7.9%; Score 102.5; DB 1; Length 235;
Best Local Similarity	24.6%; Pred. No. 0.059;

	Matches	19;	Conservative	28;	Mismatches	53;	Indels	69;	Gaps	12;
QY	104	RAVLTKQKKKKSHVLT-----	VPINATSK--DDSDVTEVMQPAL-----	RRGR	146					
Db	54	RVTGQEEEGSPNNLHLNVPVACWLTLSASRALSDKPLAHVNVANPQVEGOLQWLSDRAN			113					
QY	147	GLQAGGVAVR:OD-----	AGVYLLVSGVLFQDVTFTMGQVVSREGG-----		188					
Db	114	ALLAN--GMKRLTDQVLVPADGLVLYISQVLF-----	SGGCGRSYLLTHTV		158					
QY	189	-----ROETLTFCRISMPSH---PDR-----	YNSCSGAGVFHLHQGDIILSVIIPRA		232					
Db	159	SRFANVSNNKNNLNSAITS-PCRETPEEAEPMMAYEPYLVGCVFQLEKGRSLSTEVNQP			217					
QY	233	RAKLNLSPHG-TFLGFEVXL	250							
Db	218	E-YLDLAEISGVYFGIIL	235							
RESULT 14										
TNPF6_MACMU		STANDARD;	PRF;	280	AA.					
AC	Q9MYL6; O9BDM5;									
DT	15-JUN-2002 (Rel. 41, Created)									
DT	15-JUN-2002 (Rel. 41, Last sequence update)									
DT	15-JUN-2002 (Rel. 41, Last annotation update)									
Db	Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand) (CD95L protein).									
GN	TNFRSF6 OR FASL OR CD95L.									
OS	Macaca mulatta (Rheus macaque),									
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and									
OS	Macaca nemestrina (pig-tailed macaque).									
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;									
OC	Cercopithecoidea; Macaca.									
OX	NCBI_TaxID=9544; 9541, 9545;									
RP	[1]									
RP	SEQUENCE FROM N.A.									
RC	SPECIES=M.mulatta; TISSUE=Lymphocytes;									
RX	MEDLINE=21383618; PubMed=11491535;									
RA	Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,									
RA	Weiss W.R., Ansari A.A.;									
RT	"Cloning, sequencing, and homology analysis of nonhuman primate									
RT	Fas/Fas-ligand and co-stimulatory molecules.";									
RL	Immunogenetics 53:315-328(2001).									
RL	[2]									
RP	SEQUENCE FROM N.A.									
RC	SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;									
RA	Kiriti Y., Inoue T., Yoshino K.;									
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.									
CC	-1- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that									
CC	transduces the apoptotic signal into cells. May be involved in									
CC	cytotoxic T cell mediated apoptosis and in T cell development.									
CC	TNFRSF6/FAS-mediated apoptosis may have a role in the induction of									
CC	peripheral tolerance, in the antigen-stimulated suicide of mature									
CC	T cells, or both. Binding to the decoy receptor TNFRSF8/DCR3									
CC	modulates its effects (By similarity).									
CC	-1- SUBUNIT: Homotrimer (Potential).									
CC	-1- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By									
CC	similarity).									
CC	-1- PM: The soluble form derives from the membrane form by									
CC	proteolytic processing (By similarity).									
CC	-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.									
CC	-----									
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/									
CC	or send an email to license@isb-sib.ch).									
CC	-----									
CC	EMBL: AF344856; AAK37539.1; -									

DR EMBL; AB035138; BAA90294.1; -
 DR EMBL; AB035139; BAA90295.1; -
 DR EMBL; AB035140; BAA90296.1; -
 DR HSSP; P01375; 4TSV.
 DR InterPro; IPR003636; TNF_abc.
 DR InterPro; IPR00478; TNF_family.
 DR Pfam; PF00229; TNF; 1.
 DR PRINTS; PRO1234; TNECROSISFCT.
 DR PRODOM; PD002012; TNF_abc; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS00049; TNF_2; 1.
 DR CytoKine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
 KW CHAIN 1 280
 FT CHAIN 129 280
 FT TRANSSEM 81 101
 FT DOMAIN 1 80
 FT TRANSSEM 81 101
 FT DOMAIN 102 280
 FT DOMAIN 4 69
 FT SITE 128 129
 FT SITE 128 129
 FT DISULFID 201 232
 FT CARBOHYD 183 183
 FT CARBOHYD 249 249
 FT CARBOHYD 259 259
 FT CONFLICT 60 60
 SQ SEQUENCE 280 AA; 31367 MW; F0B284D61A132E84 CRC64;

Query Match 7.9%; Score 102.5; DB 1; Length 280;
 Best Local Similarity 22.3%; Pred. No. 0.074;
 Matches 61; Conservative 32; Mismatches 107; Indels 73; Gaps 9;

QY 2 PASSPFLAPKPPGNNMGPRREPALVALMWSGALGAVACAMALLTOOTELSLRE 61
 DB 57 PPPSPFLPPLPPLPKRGHSTGLCLLVFVVALVALGLGMFOLPHLOKELALEES 116
 QY 62 VSRLOGTGSPGNGRGYQWQSLPEQSSDALBAMENGERSRKRAVALTKOKKHSLHLV 121
 DB 117 TSQ-KHTASSLSKQIGHP--SEPP--KEQRVLAHL- 148
 QY 122 PINATSKDDSDVTEVMOP--ALRRGRGLQAGYVR1QDAGVLLYSQVLF- 171
 DB 149 ---TGKNSRSMPLMEEDTGVILSGVKYKGLVINEGLVYVSGVYRGQSCNTL 204
 QY 172 -----ODVTFMGQVVSREGQROETLFRCLNSMPSPHPRAINSCYSAGVF 217
 DB 205 PLSHKVYVRNSKYPODLVWMEGKMSYCTTGO-----MMAH-----SYLGAVF 248
 QY 218 HLHGGDILSVIIPRAKLNLSPHGTPLGFLVYL 250
 DB 249 NLTSADHLVNVSEL-SLVNFEESOTFFGLYKL 280

RESULT 15
 TNFA CEREL STANDARD; PRT; 229 AA.
 AC PS1743;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
 DE ligand superfamily member 2) (Cachectin) (Fragment).
 GN TNF OR TNFSF2 OR TNFA.
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
 OC Cervidae; Cervine; Cervus.
 CX NCBI_TaxID=9860;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Lockhart E.A.;
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
 CC TNFRSF1B/TNFR2. It is mainly secreted by macrophages and can
 CC induce cell death of certain tumor cell lines. It is potent
 CC pyrogen causing fever by direct action or by stimulation of
 CC interleukin 1 secretion and is implicated in the induction of
 CC cachexia, under certain conditions it can stimulate cell
 CC proliferation and induce cell differentiation.
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
 CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
 CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
 CC PROTEOLYTIC PROCESSING (BY SIMILARITY).
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
 CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
 CC AND MALNUTRITION.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -----
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 CC -----
 DR EMBL; U14683; AAA50759.1; -
 DR HSSP; P01375; 4TSV.
 DR InterPro; IPR003636; TNF_abc.
 DR InterPro; IPR00478; TNF_family.
 DR Pfam; PF00229; TNF; 1.
 DR PRODOM; PD002012; TNF_abc; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS00049; TNF_2; 1.
 DR CytoKine; Cyclooxin; Transmembrane; Signal-anchor.
 KW CHAIN 1 229
 FT CHAIN <1 229
 FT CHAIN 74 229
 FT DOMAIN <1 30
 FT TRANSSEM 31 51
 FT DOMAIN 52 229
 FT SITE 72 73
 FT DISULFID 141 173
 SQ SEQUENCE 229 AA; 24987 MW; 16DE5F7AA5A7DB35 CRC64;

Query Match 7.7%; Score 100; DB 1; Length 229;
 Best Local Similarity 29.4%; Pred. No. 0.095;
 Matches 48; Conservative 24; Mismatches 39; Indels 52; Gaps 13;

QY 106 VLTKOKKHNS---VHLVLP-INATSKDDSDVTEVMOPALRRGRGLQAGYVR1QD- 159
 DB 70 VQTLRSSQASINKPVAHVANINAQC-----QLMLDSC--ANALMAN--GVKLEDN 118
 QY 160 -----AGVLLYSQVLFOD-----VTFMGQV-VSREGQROETLFRCLNSMPSH 203
 DB 119 QLVVPTDGLVLYISQVLFPRGQSCSTPLFLHTISRLAVSYQ---TKNIIAALKS-PCH 174
 QY 204 ---PDRA-----YNSCYSAGVFHLHGGDILSVIIPRAKLNLS 238
 DB 175 RETPEWMAEKWPYEPYIOGGVFOLEKGDRLS-----AEINL 210

Search completed: March 26, 2003, 07:31:58
 Job time : 12 secs

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OM protein - protein search, using sw model

Run on: March 26, 2003, 07:45:50 ; Search time 28 Seconds

(without alignments)
262.705 Million cell updates/sec

Title: US-09-724-341-8

Perfect score: 250
Sequence: 1 MPASSPFLAPKCPGPMGCG.....RARKNLSPHGTFGLGVKL 250Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

d size: 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database:

Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	250	100.0	250	4	US-08-883-086-2
2	246	98.4	247	4	US-09-157-864-4
3	183	73.2	250	4	US-09-157-927-4
4	162	64.8	205	4	US-09-286-529-5
5	147	58.8	147	4	US-08-883-086-3
6	136	54.4	136	4	US-09-589-287B-20
7	121	48.4	234	4	US-09-157-864-2
8	18	7.2	24	4	US-09-157-864-6
9	10	4.0	16	4	US-09-157-864-8
10	7	2.8	31	4	US-09-181-941-13
11	7	2.8	62	1	US-09-615-192A-300
12	7	2.8	101	3	US-09-034-916-4
13	7	2.8	145	4	US-09-286-529-21
14	7	2.8	155	4	US-09-589-287B-23
15	7	2.8	179	4	US-09-615-192A-299
16	7	2.8	219	4	US-09-589-287B-28
17	7	2.8	219	4	US-09-589-287B-30
18	7	2.8	266	4	US-09-589-287B-19
19	7	2.8	285	4	US-09-286-529-1
20	7	2.8	285	4	US-09-589-287B-2
21	7	2.8	389	4	US-09-589-287B-38
22	7	2.8	336	1	US-08-414-926A-26
23	7	2.8	336	2	US-08-926-922-26
24	7	2.8	336	3	US-09-253-682-26
25	7	2.8	336	4	US-09-527-657-26
26	7	2.8	346	3	US-09-034-916-2
27	7	2.8	364	1	US-08-400-422-3

28	7	2.8	401	4	US-09-462-645C-2	Sequence 2, Appli
29	7	2.8	401	4	US-09-462-645C-6	Sequence 6, Appli
30	7	2.8	401	4	US-09-462-645C-10	Sequence 10, Appli
31	7	2.8	724	4	US-09-562-737-29	Sequence 29, Appli
32	7	2.8	1090	3	US-08-307-896-3	Sequence 3, Appli
33	7	2.8	1090	3	US-08-726-214-4	Sequence 4, Appli
34	7	2.8	1090	5	PCT-US95-11808-3	Sequence 1, Appli
35	7	2.8	1891	2	US-08-804-227C-12	Sequence 12, Appli
36	7	2.8	1891	2	US-08-804-198-6	Sequence 6, Appli
37	7	2.8	2627	2	US-08-751-189-3	Sequence 3, Appli
38	7	2.8	2627	2	US-09-060-836-3	Sequence 3, Appli
39	7	2.8	2627	4	US-09-184-445-3	Sequence 4, Appli
40	7	2.8	2629	2	US-08-751-189-4	Sequence 4, Appli
41	7	2.8	2629	2	US-09-060-836-4	Sequence 4, Appli
42	7	2.8	2629	4	US-09-184-445-4	Sequence 4, Appli
43	7	2.8	4150	4	US-09-428-517-2	Sequence 2, Appli
44	6	2.4	15	1	US-08-107-235-10	Sequence 10, Appli
45	6	2.4	15	1	US-08-178-268-4	Sequence 4, Appli
46	6	2.4	15	3	US-08-714-560B-10	Sequence 10, Appli
47	6	2.4	15	4	US-09-598-784-10	Sequence 10, Appli
48	6	2.4	15	4	US-09-009-953-142	Sequence 142, App
49	6	2.4	16	4	US-09-157-864-7	Sequence 7, Appli
50	6	2.4	17	4	US-09-162-681C-119	Sequence 119, App
51	6	2.4	22	4	US-08-690-775-1	Sequence 1, Appli
52	6	2.4	23	1	US-07-987-286-3	Sequence 3, Appli
53	6	2.4	23	2	US-08-614-626-3	Sequence 3, Appli
54	6	2.4	25	1	US-07-987-286-3	Sequence 11, Appli
55	6	2.4	25	1	US-07-987-286-24	Sequence 24, Appli
56	6	2.4	25	2	US-08-614-626-11	Sequence 11, Appli
57	6	2.4	25	2	US-08-614-626-24	Sequence 24, Appli
58	6	2.4	25	4	US-09-230-548-20	Sequence 20, Appli
59	6	2.4	30	4	US-09-181-941-9	Sequence 9, Appli
60	6	2.4	33	4	US-09-181-941-14	Sequence 14, Appli
61	6	2.4	51	4	US-09-369-994-16	Sequence 16, Appli
62	6	2.4	51	4	US-09-358-659D-14	Sequence 14, Appli
63	6	2.4	59	4	US-09-655-270A-30	Sequence 30, Appli
64	6	2.4	86	4	US-09-247-155-112	Sequence 112, App
65	6	2.4	96	2	US-08-710-749-28	Sequence 28, Appli
66	6	2.4	106	4	US-08-469-260A-253	Sequence 253, App
67	6	2.4	122	4	US-09-199-637A-353	Sequence 353, App
68	6	2.4	127	4	US-08-858-207A-490	Sequence 490, App
69	6	2.4	129	4	US-09-189-637A-371	Sequence 371, App
70	6	2.4	139	1	US-07-994-669A-10	Sequence 10, Appli
71	6	2.4	142	2	US-08-997-080-47	Sequence 47, Appli
72	6	2.4	142	2	US-08-973-970-47	Sequence 47, Appli
73	6	2.4	142	3	US-08-883-086-2	Sequence 47, Appli
74	6	2.4	142	4	US-09-095-855-47	Sequence 47, Appli
75	6	2.4	142	4	US-08-705-547A-47	Sequence 47, Appli
76	6	2.4	142	4	US-09-324-542-47	Sequence 47, Appli
77	6	2.4	142	4	US-09-205-426-47	Sequence 47, Appli
78	6	2.4	142	4	US-09-200-643-47	Sequence 47, Appli
79	6	2.4	145	1	US-07-994-669A-9	Sequence 9, Appli
80	6	2.4	147	1	US-07-668-517-1	Sequence 1, Appli
81	6	2.4	147	4	US-09-105-543A-9	Sequence 9, Appli
82	6	2.4	148	1	US-07-668-517-2	Sequence 2, Appli
83	6	2.4	148	1	US-07-668-517-15	Sequence 15, Appli
84	6	2.4	148	4	US-09-724-664-41	Sequence 41, Appli
85	6	2.4	149	1	US-07-668-517-3	Sequence 3, Appli
86	6	2.4	149	1	US-07-668-517-16	Sequence 16, Appli
87	6	2.4	150	1	US-07-668-517-4	Sequence 4, Appli
88	6	2.4	150	1	US-07-668-517-5	Sequence 5, Appli
89	6	2.4	150	1	US-07-668-517-6	Sequence 6, Appli
90	6	2.4	150	1	US-07-668-517-8	Sequence 8, Appli
91	6	2.4	150	1	US-07-668-517-9	Sequence 9, Appli
92	6	2.4	150	1	US-07-668-517-10	Sequence 10, Appli
93	6	2.4	150	1	US-07-668-517-11	Sequence 11, Appli
94	6	2.4	150	1	US-07-668-517-12	Sequence 12, Appli
95	6	2.4	150	1	US-07-668-517-13	Sequence 13, Appli
96	6	2.4	150	1	US-07-668-517-14	Sequence 14, Appli
97	6	2.4	150	1	US-07-668-517-17	Sequence 17, Appli
98	6	2.4	150	1	US-07-668-517-29	Sequence 29, Appli
99	6	2.4	150	1	US-07-668-517-31	Sequence 31, Appli
100	6	2.4	150	1	US-07-668-517-35	Sequence 35, Appli

ALIGNMENTS

RESULT 1
US-08-883-086-2

; Sequence 2, Application US/08883086
; Patent No. 6171787
; GENERAL INFORMATION:
; APPLICANT: WILEY, STEVEN
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,086
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Potembski, Priscilla E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 6134, US .01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-937-0378
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6171787e
; -08-883-086-2

Query Match 100.0%; Score 250; DB 4; Length 250;
Best Local Similarity 100.0%; Pred. No. 1e-231;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPASSPFLAPKGPNNMGVPVREPALSVLWLSMGALGAVACAMALLTQOTELQSLRR 60
DB 1 MPASSPFLAPKGPNNMGVPVREPALSVLWLSMGALGAVACAMALLTQOTELQSLRR 60
QY 61 EVSRLQGTGSPQNGEGYPMQSLPEQSSDALAEWNGERSRKRRAVLTQKKQKHSVLHL 120
DB 61 EVSRLQGTGSPQNGEGYPMQSLPEQSSDALAEWNGERSRKRRAVLTQKKQKHSVLHL 120
QY 61 EVSRLQGTGSPQNGEGYPMQSLPEQSSDALAEWNGERSRKRRAVLTQKKQKHSVLHL 120
DB 61 EVSRLQGTGSPQNGEGYPMQSLPEQSSDALAEWNGERSRKRRAVLTQKKQKHSVLHL 120
QY 121 VPINATSKDSDVTEVMQPALRRGGLQAGYGVRIODAGVYLLYSQVLFQDVTFTMGQ 180
DB 121 VPINATSKDSDVTEVMQPALRRGGLQAGYGVRIODAGVYLLYSQVLFQDVTFTMGQ 180
QY 181 VVSREGQROETLFRCTIRSMPSHPDRAVNSCYSAVFHLHOGDILSVIIPARAKLNLSP 240
DB 181 VVSREGQROETLFRCTIRSMPSHPDRAVNSCYSAVFHLHOGDILSVIIPARAKLNLSP 240
QY 241 HGTFLGFVKL 250
DB 241 HGTFLGFVKL 250

RESULT 2
US-09-157-864-4

; Sequence 4, Application US/09157864
; Patent No. 6440694
; GENERAL INFORMATION:
; APPLICANT: Bienkowski, Michael J
; APPLICANT: Mills, Cynthia J
; APPLICANT: Jones, David A
; TITLE OF INVENTION: TNF-Related Death Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
; ADDRESS: Legal Services
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/157,864
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Keiber, Lori L.
; REGISTRATION NUMBER: 41,113
; REFERENCE/DOCKET NUMBER: 6111, N CNI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 616/833-0974
; TELEFAX: 616/833-8897
; TELEX: 224401
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-157-864-4

Query Match 98.4%; Score 246; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 6.7e-228;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPASSPFLAPKGPNNMGVPVREPALSVLWLSMGALGAVACAMALLTQOTELQSLRR 60
DB 1 MPASSPFLAPKGPNNMGVPVREPALSVLWLSMGALGAVACAMALLTQOTELQSLRR 60
QY 61 EVSRLQGTGSPQNGEGYPMQSLPEQSSDALAEWNGERSRKRRAVLTQKKQKHSVLHL 120
DB 61 EVSRLQGTGSPQNGEGYPMQSLPEQSSDALAEWNGERSRKRRAVLTQKKQKHSVLHL 120
QY 121 VPINATSKDSDVTEVMQPALRRGGLQAGYGVRIODAGVYLLYSQVLFQDVTFTMGQ 180
DB 121 VPINATSKDSDVTEVMQPALRRGGLQAGYGVRIODAGVYLLYSQVLFQDVTFTMGQ 180
QY 181 VVSREGQROETLFRCTIRSMPSHPDRAVNSCYSAVFHLHOGDILSVIIPARAKLNLSP 240
DB 181 VVSREGQROETLFRCTIRSMPSHPDRAVNSCYSAVFHLHOGDILSVIIPARAKLNLSP 240
QY 241 HGTFLG 246
DB 241 HGTFLG 246
RESULT 3
US-09-153-927-4

; Sequence 4, Application US/09153927A
; Patent No. 6297022
; GENERAL INFORMATION:
; APPLICANT: McDONNELL, Peter C.
; APPLICANT: Young, Peter R.
; APPLICANT: Zou, Jun
; TITLE OF INVENTION: A Method of Identifying Agonists and
; TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3
; FILE OF INVENTION: and TR5
; FILE REFERENCE: GH50031
; CURRENT APPLICATION NUMBER: US/09/153,927A
; CURRENT FILING DATE: 1998-09-16
; EARLIER APPLICATION NUMBER: 60/061,334
; EARLIER FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Human
09-153-927-4

Query Match 73.2%; Score 183; DB 4; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.5e-167;
Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 TGGSPONGEGYPWQSLPEQSSDALEAMENGRSRKRAVLTQKQKHSHLVLPINATS 127
DB 68 TGGSPONGEGYPWQSLPEQSSDALEAMENGRSRKRAVLTQKQKHSHLVLPINATS 127
QY 128 KDSDDVTEVMQPALRRGRGLQAGGYVRIODAGVYLLYSQVLFQDVTFTMGQVVSREGQ 187
DB 128 KDSDDVTEVMQPALRRGRGLQAGGYVRIODAGVYLLYSQVLFQDVTFTMGQVVSREGQ 187
QY 108 GROETLFRCSRMSHPDRAYNSCYSAGVFLHOGDILSVIIPARAALNLSPHGTPLGF 247
DB 108 GROETLFRCSRMSHPDRAYNSCYSAGVFLHOGDILSVIIPARAALNLSPHGTPLGF 247
QY 248 VKL 250
DB 248 VKL 250

RESULT 4
US-09-286-529-5
; Sequence 5, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catheline Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408,003/200130,439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 205
; TYPE: PRT
; ORGANISM: human
US-09-286-529-5

Query Match 64.8%; Score 162; DB 4; Length 205;
Best Local Similarity 100.0%; Pred. No. 1.6e-147;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 LTOQTEIQLREVSRLOGTGGSPONGEGYPWQSLPEQSSDALEAMENGRSRKRAVLT 108
DB 4 LTOQTEIQLREVSRLOGTGGSPONGEGYPWQSLPEQSSDALEAMENGRSRKRAVLT 63
QY 109 QKQKHSHLVLPINATSKDSDVTEVMQPALRRGRGLQAGGYVRIODAGVYLLYSQ 168
DB 64 QKQKHSHLVLPINATSKDSDVTEVMQPALRRGRGLQAGGYVRIODAGVYLLYSQ 123

QY 169 VLFQDVTFTMGQVVSREGQROETLFRCSRMSHPDRAYNS 210
DB 124 VLFQDVTFTMGQVVSREGQROETLFRCSRMSHPDRAYNS 165

RESULT 5
US-08-883-086-3
; Sequence 3, Application US/08883086
; Patent No. 6171787
; GENERAL INFORMATION:
; APPLICANT: WILEY, STEVEN
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,086
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Potembski, Priscilla E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 6134.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-937-0378
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 147 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6171787e
US-08-883-086-3

Query Match 58.8%; Score 147; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 2.8e-133;
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 RAVLTQKQKHSHLVLPINATSKDSDVTEVMQPALRRGRGLQAGGYVRIODAGVY 163
DB 1 RAVLTQKQKHSHLVLPINATSKDSDVTEVMQPALRRGRGLQAGGYVRIODAGVY 60
QY 164 LLYSQVLFQDVTFTMGQVVSREGQROETLFRCSRMSHPDRAYNSCYSAGVFLHOGD 223
DB 61 LLYSQVLFQDVTFTMGQVVSREGQROETLFRCSRMSHPDRAYNSCYSAGVFLHOGD 120
QY 224 ILSVIIPARAALNLSPHGTPLGFVKL 250
DB 121 ILSVIIPARAALNLSPHGTPLGFVKL 147

RESULT 6
US-09-589-287B-20
; Sequence 20, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.

```

: TITLE OF INVENTION: Antibodies to Neutrokin-alpha
: FILE REFERENCE: PF343P3C1
: CURRENT APPLICATION NUMBER: US/09/589,287B
: CURRENT FILING DATE: 2000-06-08
: Prior application data removed - check PALM or file wrapper
: NUMBER OF SEQ ID NOS: 42
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 20
: LENGTH: 136
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-589-287B-20

Query Match          54.4%; Score 136; DB 4; Length 136;
Best Local Similarity 100.0%; Pred. No. 9e-123;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 HSVLHLPINATSKDSDVTEVMQPALRRGRLQAGYGVRIQDAGVYLLYSQVLFQDV 174
1 HSVLHLPINATSKDSDVTEVMQPALRRGRLQAGYGVRIQDAGVYLLYSQVLFQDV 60
175 TPTMGQVVSREGQGRQETLFRICIRSMPSHPDRAVNSCSAGVFHLHQGDILSVIIPRARA 234
DB 61 TPTMGQVVSREGQGRQETLFRICIRSMPSHPDRAVNSCSAGVFHLHQGDILSVIIPRARA 120

QY 235 KLNLSPHGTFILGFVKL 250
DB 121 KLNLSPHGTFILGFVKL 136

RESULT 7
US-09-157-864-2
: Sequence 2, Application US/09157864
: Patent No. 6440694
: GENERAL INFORMATION:
: APPLICANT: Bienkowski, Michael J
: APPLICANT: Mills, Cynthia J
: APPLICANT: Jones, David A
: TITLE OF INVENTION: TNF-Related Death Ligand
: NUMBER OF SEQUENCES: 18
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
: ADDRESSEE: Legal Services
: STREET: 301 Henrietta Street
: CITY: Kalamazoo
: STATE: MI
: COUNTRY: USA
: ZIP: 49001
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 Diskette
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/157,864
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Kerber, Lori L.
: REGISTRATION NUMBER: 41,113
: REFERENCE/DOCKET NUMBER: 6111.N CN1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 616/833-0974
: TELEFAX: 616/833-8897
: TELEX: 224401
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 234 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-09-157-864-2

```

```

Query Match          48.4%; Score 121; DB 4; Length 234;
Best Local Similarity 100.0%; Pred. No. 3.4e-108;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 DSDVTEVMQPALRRGRLQAGYGVRIQDAGVYLLYSQVLFQDVTTMGQVVSREGQGR 189
DB 114 DSDVTEVMQPALRRGRLQAGYGVRIQDAGVYLLYSQVLFQDVTTMGQVVSREGQGR 173

QY 190 QETLFRICIRSMPSHPDRAVNSCSAGVFHLHQGDILSVIIPRARKLNLSPHGTFILGFVK 249
DB 174 QETLFRICIRSMPSHPDRAVNSCSAGVFHLHQGDILSVIIPRARKLNLSPHGTFILGFVK 233

QY 250 L 250
DB 234 L 234

RESULT 8
US-09-157-864-6
: Sequence 6, Application US/09157864
: Patent No. 6440694
: GENERAL INFORMATION:
: APPLICANT: Bienkowski, Michael J
: APPLICANT: Mills, Cynthia J
: APPLICANT: Jones, David A
: TITLE OF INVENTION: TNF-Related Death Ligand
: NUMBER OF SEQUENCES: 18
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
: ADDRESSEE: Legal Services
: STREET: 301 Henrietta Street
: CITY: Kalamazoo
: STATE: MI
: COUNTRY: USA
: ZIP: 49001
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 Diskette
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/157,864
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Kerber, Lori L.
: REGISTRATION NUMBER: 41,113
: REFERENCE/DOCKET NUMBER: 6111.N CN1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 616/833-0974
: TELEFAX: 616/833-8897
: TELEX: 224401
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 24 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-09-157-864-6

Query Match          7.2%; Score 18; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 AGVFHLHQGDILSVIIPR 211
DB 7 AGVFHLHQGDILSVIIPR 24

RESULT 9
US-09-157-864-8

```


Sequence 8, Application US/09157864
Patent No. 6440694
GENERAL INFORMATION:
APPLICANT: Bienkowski, Michael J
APPLICANT: Mills, Cynthia J
APPLICANT: Jones, David A
TITLE OF INVENTION: TNF-Related Death Ligand
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
STREET: 301 Henrietta Street
CITY: Kalamazoo
STATE: MI
COUNTRY: USA
ZIP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09157,864
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Keider, Lori L.
REGISTRATION NUMBER: 41,113
REFERENCE/DOCKET NUMBER: 6111.N.CN1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616/833-0974
TELEFAX: 616/833-8897
TELEX: 224401
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-157-864-8

Query Match 4.0%; Score 10; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 157 IODAGVLYL 166
1 IODAGVLYL 10

RESULT 10
US-09-181-941-13
Sequence 13, Application US/09181941
Patent No. 6440690
GENERAL INFORMATION:
APPLICANT: Mor, Amram
Vouldoukis, Ioannis
Nicolais, Pierre
TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION
OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows

SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/181,941
FILING DATE: 28-Oct-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/574,701
FILING DATE: 19-DEC-1995
APPLICATION NUMBER: FR 95 07831
FILING DATE: 29-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 3909-0021-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6440690e
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-181-941-13

Query Match 2.8%; Score 7; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 37 AALGAVA 43
Db 20 AALGAVA 26

RESULT 11
US-09-615-192A-300
Sequence 300, Application US/09615192A
Patent No. 6410718
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods for the
Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003c4U
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 300
LENGTH: 62
TYPE: PRT
ORGANISM: Eucalyptus grandis
US-09-615-192A-300

Query Match 2.8%; Score 7; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 242 GTFLGFV 248
Db 5 GTFLGFV 11

RESULT 12

US-09-034-916-4
; Sequence 4, Application US/09034916
; Patent No. 6046314
; GENERAL INFORMATION:
; APPLICANT: GEBE, JOHN A.
; APPLICANT: SIADAK, ANTHONY W.
; APPLICANT: ARUFO, ALEJANDRO A.
; TITLE OF INVENTION: SPALPHA: A NOVEL SCAVENGER RECEPTOR
; TITLE OF INVENTION: CYSTEINE-RICH DOMAIN-CONTAINING POLYPEPTIDE AND MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES THERETO
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/034,916
; FILING DATE: 04-MAR-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/039,956
; FILING DATE: 06-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5998-0020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 325-7812
; TELEFAX: (650) 325-7823
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 101 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-034-916-4

Query Match 2.8%; Score 7; DB 3; Length 101;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 104 RAVLTOK 110
Db 45 RAVLTOK 51

RESULT 13
US-09-286-529-21
; Sequence 21, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408, 003/200130, 439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-286-529-21

Query Match 2.8%; Score 7; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 209 NSCYSAG 215
Db 103 NSCYSAG 109

RESULT 14
US-09-589-287B-23
; Sequence 23, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neurokinine-alpha
; FILE REFERENCE: PR343P3C1
; CURRENT APPLICATION NUMBER: US/09/589,287B
; CURRENT FILING DATE: 2000-06-08
; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 23
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-287B-23

Query Match 2.8%; Score 7; DB 4; Length 155;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 209 NSCYSAG 215
Db 113 NSCYSAG 119

RESULT 15
US-09-615-192A-299
; Sequence 299, Application US/09615192A
; Patent No. 6410718
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilka
; TITLE OF INVENTION: Materials and Methods for the
; TITLE OF INVENTION: Modification of Plant Lignin Content
; FILE REFERENCE: 11000, 1003C4U
; CURRENT APPLICATION NUMBER: US/09/615,192A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 299
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-615-192A-299

Query Match 2.8%; Score 7; DB 4; Length 179;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 242 GTFLGFV 248
Db 16 GTFLGFV 22

RESULT 16

```
US-09-589-287B-28
; Sequence 28, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C1
; CURRENT APPLICATION NUMBER: US/09/589, 287B
; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 28
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-287B-28

Query Match
Best Local Similarity 2.8%; Score 7; DB 4; Length 219;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 NSCYSAG 215
Db 177 NSCYSAG 183

RESULT 17
US-09-589-287B-30
; Sequence 30, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C1
; CURRENT APPLICATION NUMBER: US/09/589, 287B
; CURRENT FILING DATE: 2000-06-08
; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 30
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-287B-30

Query Match
Best Local Similarity 2.8%; Score 7; DB 4; Length 219;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 NSCYSAG 215
Db 177 NSCYSAG 183

RESULT 18
US-09-589-287B-19
; Sequence 19, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C1
; CURRENT APPLICATION NUMBER: US/09/589, 287B
; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 19
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-287B-19
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Query Match
Best Local Similarity 2.8%; Score 7; DB 4; Length 266;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 NSCYSAG 215
Db 224 NSCYSAG 230

RESULT 19
US-09-286-529-1
; Sequence 1, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 285
; TYPE: PRT
; ORGANISM: human
US-09-286-529-1

Query Match
Best Local Similarity 2.8%; Score 7; DB 4; Length 285;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 NSCYSAG 215
Db 243 NSCYSAG 249

RESULT 20
US-09-589-287B-2
; Sequence 2, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C1
; CURRENT APPLICATION NUMBER: US/09/589, 287B
; CURRENT FILING DATE: 2000-06-08
; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 2
; LENGTH: 285
; TYPE: PRT
; ORGANISM: human
US-09-589-287B-2

Query Match
Best Local Similarity 2.8%; Score 7; DB 4; Length 285;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 NSCYSAG 215
Db 243 NSCYSAG 249

RESULT 21
US-09-589-287B-38
; Sequence 38, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C1
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;; CURRENT APPLICATION NUMBER: US/09/589,287B
;; CURRENT FILING DATE: 2000-06-08
;; Prior application data removed - check PALM or file wrapper
;; NUMBER OF SEQ ID NOS: 42
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 38
;; LENGTH: 289
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-09-589-287B-38

Query Match 2.8%; Score 7; DB 4; Length 289;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 209 NSCVSAG 215
DB 247 NSCVSAG 253

SUT 22
-08-414-926A-26
Sequence 26, Application US/08414926A
Patent No. 5721354
GENERAL INFORMATION:
APPLICANT: Spaete, Richard
APPLICANT: Cha, Tai-An
TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,926A
FILING DATE: March 31, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: AVIR-011/OUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-494-7622
TELEFAX: 415-857-0663
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: col.22
FEATURE:
NAME/KEY: Protein
LOCATION: 1..336
OTHER INFORMATION: /label= UL151
US-08-414-926A-26

Query Match 2.8%; Score 7; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 142 LRRGRL 148
DB 82 LRRGRL 88

RESULT 23
US-08-926-922-26

Sequence 26, Application US/08926922
Patent No. 5925751
GENERAL INFORMATION:
APPLICANT: Spaete, Richard
APPLICANT: Cha, Tai-An
TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Luann Cserr Attorney at Law
STREET: 750 Arimo Avenue
CITY: Oakland
STATE: CA
COUNTRY: USA
ZIP: 94610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,922
FILING DATE: September 10, 1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: AVIR 11A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-834-1448
TELEFAX: 510-839-7810
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: col.22
FEATURE:
NAME/KEY: Protein
LOCATION: 1..336
OTHER INFORMATION: /label= UL151
US-08-926-922-26

Query Match 2.8%; Score 7; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 142 LRRGRL 148
DB 82 LRRGRL 88

RESULT 24
US-09-253-682-26
Sequence 26, Application US/09253682
Patent No. 6040170
GENERAL INFORMATION:
APPLICANT: Spaete, Richard
APPLICANT: Cha, Tai-An
TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Luann Cserr Attorney at Law
STREET: 750 Arimo Avenue
CITY: Oakland
STATE: CA
COUNTRY: USA
ZIP: 94610

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/253,682
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/926,922
; FILING DATE: September 10, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Geert, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR 11A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-834-1448
; TELEFAX: 510-839-7810
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: col.22
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..336
; OTHER INFORMATION: /label= UL151
; US-09-253-682-26

Query Match      2.8%; Score 7; DB 3; Length 336;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 LRRGRGL 148
   |||||
Db 82 LRRGRGL 88

RESULT 25
US-09-527-657-26
; Sequence 26, Application US/09527657
; Patent No. 6291236
; GENERAL INFORMATION:
; APPLICANT: Spaete, Richard
; Cha, Tai-An
; TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
; NUMBER OF SEQUENCES: 27
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/527,657
; FILING DATE: 17-Mar-2000
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,922
; FILING DATE: September 10, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Geert, Luann
; REGISTRATION NUMBER: 31,822
```

```

; REFERENCE/DOCKET NUMBER: AVIR 11A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-834-1448
; TELEFAX: 510-839-7810
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: col.22
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..336
; OTHER INFORMATION: /label= UL151
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
; US-09-527-657-26

Query Match      2.8%; Score 7; DB 4; Length 336;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 LRRGRGL 148
   |||||
Db 82 LRRGRGL 88

RESULT 26
US-09-034-916-2
; Sequence 2, Application US/09034916
; Patent No. 6046314
; GENERAL INFORMATION:
; APPLICANT: GEEB, JOHN A.
; APPLICANT: SIADAK, ANTHONY W.
; APPLICANT: ARUFFO, ALEJANDRO A.
; TITLE OF INVENTION: SPALPHA: A NOVEL SCAVENGER RECEPTOR
; TITLE OF INVENTION: CYSTEINE-RICH DOMAIN-CONTAINING POLYPEPTIDE AND MONOCLONAL
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/034,916
; FILING DATE: 04-MAR-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/039,956
; FILING DATE: 06-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5998-0020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 325-7812
; TELEFAX: (650) 325-7823
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-034-916-2
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Query Match 2.8%; Score 7; DB 3; Length 346;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 RAVLTOK 110
Db 182 RAVLTOK 188

RESULT 27
US-08-400-422-3
Sequence 3, Application US/08400422
Patent No. 5681715
GENERAL INFORMATION:
APPLICANT: Jorgensen, Steen Troels
APPLICANT: Diderichsen, Borge Krag
APPLICANT: Buckley, Catherine M.
APPLICANT: Hobson, Audrey
APPLICANT: McConnell, David J.
TITLE OF INVENTION: A process for the preparation of an active
TITLE OF INVENTION: lipase
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56817150 No. 5681715disk of No. 5681715th America, Inc.
STREET: 405 Lexington Avenue, 62nd floor
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400.422
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/038.763
FILING DATE: 25-MAR-1993
APPLICATION NUMBER: PCT/DK91/00402
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK92/00391
FILING DATE: 18-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3663.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Pseudomonas cepacia
STRAIN: DSM 3401
US-08-400-422-3

Query Match 2.8%; Score 7; DB 1; Length 364;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GAVACAM 46
Db 12 GAVACAM 18

RESULT 28
US-09-462-645C-2
Sequence 2, Application US/09462645C
Patent No. 6436681
GENERAL INFORMATION:
APPLICANT: Schroeder, Hartwig
APPLICANT: Hauer, Bernhard
TITLE OF INVENTION: The preparation of biotin
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/462.645C
CURRENT FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: PCT/EP98/04097
PRIOR FILING DATE: 1998-02-07
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Wordperfect version 6.1
SEQ ID NO 2
LENGTH: 401
TYPE: PRT
ORGANISM: E. Coli w3110
US-09-462-645C-2

Query Match 2.8%; Score 7; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 QDAGVYL 164
Db 17 QDAGVYL 23

RESULT 29
US-09-462-645C-6
Sequence 6, Application US/09462645C
Patent No. 6436681
GENERAL INFORMATION:
APPLICANT: Schroeder, Hartwig
APPLICANT: Hauer, Bernhard
TITLE OF INVENTION: The preparation of biotin
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/462.645C
CURRENT FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: PCT/EP98/04097
PRIOR FILING DATE: 1998-02-07
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Wordperfect version 6.1
SEQ ID NO 6
LENGTH: 401
TYPE: PRT
ORGANISM: clone pHSibios1
US-09-462-645C-6

Query Match 2.8%; Score 7; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 158 QDAGVYL 164
Db 17 QDAGVYL 23

RESULT 30
US-09-462-645C-10
Sequence 10, Application US/09462645C
Patent No. 6436681
GENERAL INFORMATION:
APPLICANT: Schroeder, Hartwig
APPLICANT: Hauer, Bernhard
TITLE OF INVENTION: The preparation of biotin

FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/462,645C
CURRENT FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: PCT/EP98/04097
PRIOR FILING DATE: 1998-02-07
NUMBER OF SEQ ID NOS: 38
SOFTWARE: WordPerfect version 6.1
SEQ ID NO 10
LENGTH: 401
TYPE: PRT
ORGANISM: clone pHS2bioS1
US-09-462-645C-10

Query Match 2.8%; Score 7; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 158 ODAGVYL 164
DB 17 ODAGVYL 23

RESULT 31
US-09-562-737-29
Sequence 29, Application US/09562737
Patent No. 6428967
GENERAL INFORMATION:
APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 29
LENGTH: 724
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-562-737-29

Query Match 2.8%; Score 7; DB 4; Length 724;
Best Local Similarity 100.0%; Pred. No. 1,5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 59 RREVSRL 65
DB 496 RREVSRL 502

RESULT 32
US-08-307-896-3
Sequence 3, Application US/08307896C
Patent No. 6034071
GENERAL INFORMATION:
APPLICANT: Iyengar, Srinivas Ravi
TITLE OF INVENTION: MUTANT ACTIVATED GSALPHA AND ADENYLYL
FILE REFERENCE: 29770
CURRENT APPLICATION NUMBER: US/08/307,896C
CURRENT FILING DATE: 1994-09-16
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 1090
TYPE: PRT
ORGANISM: Rattus norvegicus
US-08-307-896-3

Query Match 2.8%; Score 7; DB 3; Length 1090;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 166 YSOVLFO 172
DB 787 YSOVLFO 793

RESULT 33
US-08-726-214-4
Sequence 4, Application US/08726214
Patent No. 6107076
GENERAL INFORMATION:
APPLICANT: Tang, Wei-Jen
APPLICANT: Gilman, Alfred G.
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,214
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,498
FILING DATE: 04-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTS0:450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 474-7577
FAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1090 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-726-214-4

Query Match 2.8%; Score 7; DB 3; Length 1090;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 166 YSOVLFO 172
DB 787 YSOVLFO 793

RESULT 34
PCT-US95-11808-3
Sequence 3, Application PC/TUS9511808
GENERAL INFORMATION:
APPLICANT: Iyengar, Srinivas Ravi V.
TITLE OF INVENTION: MUTANT ACTIVATED GSALPHA AND
TITLE OF INVENTION: ADENYLYL
TITLE OF INVENTION: CYCLASE 2 FOR USE AS THERAPEUTIC AGENTS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue and
ADDRESSEE: Raymond

STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.
ZIP: 10112-0228
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11808
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,896
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Richard S.
REGISTRATION NUMBER: 26,154
REFERENCE/DOCKET NUMBER: 29970 165/28755
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-2500
TELEFAX: (212) 765-2519
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1090 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-11808-3

Query Match 2.8%; Score 7; DB 5; length 1090;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 166 YSQVLFQ 172
|||
Db 787 YSQVLFQ 793

RESULT 35
US-08-804-227C-12
Sequence 12 Application US/08804227C
Patent No. 5876991
GENERAL INFORMATION:
APPLICANT: Dehoff, Bradley S.
APPLICANT: Kuhnstoss, Stuart A.
APPLICANT: Rosbeck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: February 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-8231

TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1891 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-804-227C-12

Query Match 2.8%; Score 7; DB 2; length 1891;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 140 PALRRGR 146
|||
Db 878 PALRRGR 884

RESULT 36
US-08-804-198-6
Sequence 6 Application US/08804198
Patent No. 5945320
GENERAL INFORMATION:
APPLICANT: Burgelt, Stanley G.
APPLICANT: Kuhnstoss, Stuart A.
APPLICANT: Rao, Nagaraja R.
APPLICANT: Richardson, Mark A.
APPLICANT: Rosbeck, Paul R., Jr.
TITLE OF INVENTION: PLATENOIDE SYNTHASE GENE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: PAUL R. CANTRELL 1138
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
STATE: IN
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,198
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
REFERENCE/DOCKET NUMBER: P9113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1891 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-804-198-6

Query Match 2.8%; Score 7; DB 2; length 1891;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 140 PALRRGR 146
|||
Db 878 PALRRGR 884

RESULT 37
US-08-751-189-3
Sequence 3 Application US/08751189


```
Patent No. 5919656
GENERAL INFORMATION:
APPLICANT: Harrington, Lea A.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 5919656e1 Genes Encoding Telomerase Protein
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESS: Amgen, Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,189
FILING DATE: 15-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-433
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2627 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-751-189-3

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 2627;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 PALSVL 31
DB 1929 PALSVL 1935

RESULT 38
US-09-060-836-3
Sequence 3, Application US/09060836
Patent No. 5981707
GENERAL INFORMATION:
APPLICANT: Harrington, Lea A.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 5981707e1 Genes Encoding Telomerase Protein
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESS: Amgen, Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,836
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/751,189
```

```
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-433
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2627 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-060-836-3

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 2627;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 PALSVL 31
DB 1929 PALSVL 1935

RESULT 39
US-09-184-445-3
Sequence 3, Application US/09184445
Patent No. 6174703
GENERAL INFORMATION:
APPLICANT: Harrington, Lea A.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 6174703e1 Genes Encoding Telomerase Protein
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESS: Amgen, Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/184,445
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/751,189
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-433
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2627 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-184-445-3

Query Match
Best Local Similarity 100.0%; Score 7; DB 4; Length 2627;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 PALSVL 31
DB 1929 PALSVL 1935
```

RESULT 40
US-08-751-189-4
Sequence 4, Application US/08751189
Patent No. 5919656
GENERAL INFORMATION:
APPLICANT: Harrington, Lea A.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 5919656el Genes Encoding Telomerase Protein
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen, Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,189
CLASSIFICATION: 435
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olecki, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-433
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2629 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-751-189-4

Query Match 2.8%; Score 7; DB 2; Length 2629;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25 PALSVAL 31
Db 1936 PALSVAL 1942

SULT 41
US-09-060-836-4
Sequence 4, Application US/09060836
Patent No. 5981707
GENERAL INFORMATION:
APPLICANT: Harrington, Lea A.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 5981707el Genes Encoding Telomerase Protein
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen, Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,836

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/751,189
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olecki, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-433
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2629 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-060-836-4

Query Match 2.8%; Score 7; DB 2; Length 2629;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25 PALSVAL 31
Db 1936 PALSVAL 1942

RESULT 42
US-09-184-445-4
Sequence 4, Application US/09184445
Patent No. 6174703
GENERAL INFORMATION:
APPLICANT: Harrington, Lea A.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 6174703el Genes Encoding Telomerase Protein
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen, Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/184,445
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/751,189
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olecki, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-433
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2629 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-184-445-4

Query Match 2.8%; Score 7; DB 4; Length 2629;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25 PALSVAL 31
|||||
Db 1936 PALSVAL 1942

RESULT 43

US-09-428-517-2
; Sequence 2, Application US/09428517
; Patent No. 6251636
; GENERAL INFORMATION:
; APPLICANT: Beclach, Mary C.
; APPLICANT: McDaniel, Robert
; APPLICANT: Tang, Li
; TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
; FILE REFERENCE: 30062-20029.00
; CURRENT APPLICATION NUMBER: US/09/428,517
; CURRENT FILING DATE: 1999-10-28
; EARLIER APPLICATION NUMBER: 60/120,254
; EARLIER FILING DATE: 1999-02-16
; EARLIER APPLICATION NUMBER: 60/106,100
; EARLIER FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4150
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant
; OTHER INFORMATION: Oleandolide PKS
US-09-428-517-2

Query Match 2.8%; Score 7; DB 4; Length 4150;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 140 PALRRGR 146
|||||
Db 882 PALRRGR 888

RESULT 44

US-08-107-235-10
; Sequence 10, Application US/08107235
; Patent No. 5587457
; GENERAL INFORMATION:
; APPLICANT: Rathjen, Deborah A
; APPLICANT: Ferrante, Antonio
; APPLICANT: Widmer, Fred
; TITLE OF INVENTION: Neutrophil Stimulating Peptides
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 S. Wacker Dr.
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,235
; FILING DATE: 16-AUG-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,415
; FILING DATE: 12-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J

REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,622A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
OTHER INFORMATION: /note= "PEPTIDE 308 (54-68)"

US-08-107-235-10

Query Match 2.4%; Score 6; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 166 YSOVLF 171
|||||
Db 6 YSOVLF 11

RESULT 45

US-08-178-268-44
; Sequence 44, Application US/08178268
; Patent No. 5795859
; GENERAL INFORMATION:
; APPLICANT: RATHJEN, Deborah A
; APPLICANT: WIDMER, Fred
; APPLICANT: GRIGG, Geoffrey W
; APPLICANT: MACK, Philip O
; TITLE OF INVENTION: Peptide which Abrogates TNF and/or LPS Toxicity
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye P.C.
; STREET: 1100 No. 5795859th Glebe Road, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/178,268
; FILING DATE: 05-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: MITCHARD, Leonard C
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 47-45
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: both
MOLECULE TYPE: peptide
US-08-178-268-44

Query Match 2.4%; Score 6; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 166 YSQVLF 171
Db 6 YSQVLF 11

RESULT 46
US-08-714-960B-10
; Sequence 10, Application US/08714960B
; Patent No. 6121237
; GENERAL INFORMATION:
; APPLICANT: RATHJEN, Deborah A
; APPLICANT: FERRANTE, Antonio
; TITLE OF INVENTION: Neutrophil Stimulating Peptides
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & WITCOFF, LTD.
; STREET: 10 S. Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb storage diskette, 3.50 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: IBM compatible PC/MS-DOS
; SOFTWARE: WordPerfect version 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/714,960B
; FILING DATE: 17-SEP-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU P39065
; FILING DATE: 12-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU91/00086
; FILING DATE: 12-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,415
; FILING DATE: 09-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/107,235
; FILING DATE: 16-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Resis, Robert H.
; REGISTRATION NUMBER: 32,168
; REFERENCE/DOCKET NUMBER: 92,622-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 715-1234
; TELEFAX: (312) 715-1000
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
; OTHER INFORMATION: /note= "PEPTIDE 308 (54-68)"
; US-08-714-960B-10

Query Match 2.4%; Score 6; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 166 YSQVLF 171
Db 6 YSQVLF 11
RESULT 47
US-09-598-784-10

; Sequence 10, Application US/09598784
; Patent No. 6375928
; GENERAL INFORMATION:
; APPLICANT: RATHJEN, Deborah A
; APPLICANT: FERRANTE, Antonio
; TITLE OF INVENTION: Neutrophil Stimulating Peptides
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & WITCOFF, LTD.
; STREET: 10 S. Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb storage diskette, 3.50 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: IBM compatible PC/MS-DOS
; SOFTWARE: WordPerfect version 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/598,784
; FILING DATE: 21-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU P39065
; FILING DATE: 12-MAR-1990
; APPLICATION NUMBER: PCT/AU91/00086
; FILING DATE: 12-MAR-1991
; APPLICATION NUMBER: US 07/930,415
; FILING DATE: 09-NOV-1992
; APPLICATION NUMBER: US 08/107,235
; FILING DATE: 16-AUG-1993
; APPLICATION NUMBER: US 08/714,960
; FILING DATE: 17-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Resis, Robert H.
; REGISTRATION NUMBER: 32,168
; REFERENCE/DOCKET NUMBER: 11341.00001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 715-1000
; TELEFAX: (312) 715-1234
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
; OTHER INFORMATION: /note= "PEPTIDE 308 (54-68)"
; US-09-598-784-10

Query Match 2.4%; Score 6; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 166 YSQVLF 171
Db 6 YSQVLF 11
RESULT 48
US-09-009-953-142
; Sequence 142, Application US/09009953
; Patent No. 6413517
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Identification of Broadly
; Reactive DR Restricted Epitopes
; NUMBER OF SEQUENCES: 274

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, Eighth Floor
;; CITY: San Francisco
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94111-3834
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: PatsEQ for Windows Version 2.0
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/009,953
;; FILING DATE: 21-Jan-1998
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/036,713
;; FILING DATE: 23-JAN-1997
;; APPLICATION NUMBER: US 60/037,432
;; FILING DATE: 07-FEB-1997
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Weber, Ellen Lauver
;; REGISTRATION NUMBER: 32,762
;; REFERENCE/DOCKET NUMBER: 018623-011520US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-576-0200
;; TELEFAX: 415-576-0300
;; TELEX: <Unknown>
;;
;; INFORMATION FOR SEQ ID NO: 142:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 142:
US-09-009-953-142
;
Query Match 2.4%; Score 6; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 5 SPFLA 10
|||
Db 1 SPFLA 6
;
SULT 49
US-09-157-864-7
; Sequence 7, Application US/09157864
; Patent No. 6440694
; GENERAL INFORMATION:
; APPLICANT: Bienkowski, Michael J
; APPLICANT: Mills, Cynthia J
; APPLICANT: Jones, David A
; TITLE OF INVENTION: TNF-Related Death Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
; ADDRESSEE: Legal Services
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/157,864

;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Kerber, Lori L.
;; REGISTRATION NUMBER: 41,113
;; REFERENCE/DOCKET NUMBER: 6111.N CN1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 616/833-0974
;; TELEFAX: 616/833-8897
;; TELEX: 224401
;;
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-09-157-864-7
;
Query Match 2.4%; Score 6; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 166 YSQVLF 171
|||
Db 10 YSQVLF 15
;
RESULT 50
US-09-342-681C-119
; Sequence 119, Application US/09342681C
; Patent No. 6355782
; GENERAL INFORMATION:
; APPLICANT: Zonana et al.
; TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
; FILE REFERENCE: 52978
; CURRENT APPLICATION NUMBER: US/09/342,681C
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/092,279
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/112,366
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 119
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-342-681C-119
;
Query Match 2.4%; Score 6; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 166 YSQVLF 171
|||
Db 12 YSQVLF 17
;
RESULT 51
US-08-690-775-1
; Sequence 1, Application US/08690775
; Patent No. 6270766
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Marc
; APPLICANT: Maini, Ravinder N.
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES AND METHOTREXATE IN
; TITLE OF INVENTION: THE TREATMENT OF AUTOIMMUNE DISEASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: TWO MILLITIA DRIVE
; CITY: LEXINGTON

STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,775
FILING DATE: 01-AUG-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/607,419
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/00462
FILING DATE: 15-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02070
FILING DATE: 06-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/958,248
FILING DATE: 08-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: KIR92-01A4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-690-775-1

Query Match 2.4%; Score 6; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 166 YSQVLF 171
Db 1 YSQVLF 6

RESULT 52
US-07-987-286-3
Sequence 3, Application 07/987286
Patent No. 5500366
GENERAL INFORMATION:
APPLICANT: RUSSELL-JONES, GREGORY J
APPLICANT: GECZY, ANDREW F
TITLE OF INVENTION: T-CELL EPITOPES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K STREET, N.W.
CITY: WASHINGTON, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 07/987,286
FILING DATE: 16-MAR-1993
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU91/00429
FILING DATE: 17-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK2361
FILING DATE: 18-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, STEPHEN A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/175/CHAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-987-286-3

Query Match 2.4%; Score 6; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 36 GALGA 41
Db 14 GALGA 19

RESULT 53
US-08-614-626-3
Sequence 3, Application US/08614626
Patent No. 5928644
GENERAL INFORMATION:
APPLICANT: RUSSELL-JONES, GREGORY J
APPLICANT: GECZY, ANDREW F
TITLE OF INVENTION: T-CELL EPITOPES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K STREET, N.W.
CITY: WASHINGTON, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/614,626
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/987,286
FILING DATE: 16-MAR-1993
APPLICATION NUMBER: PCT/AU91/00429
FILING DATE: 17-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK2361
FILING DATE: 18-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, STEPHEN A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/175/CHAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-614-626-3

Query Match 2.4%; Score 6; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 GAALGA 41
Db 14 GAALGA 19

RESULT 54
US-07-987-286-11
Sequence 11, Application 07/987286
Patent No. 5500366

GENERAL INFORMATION:

APPLICANT: RUSSELL-JONES, GREGORY J
APPLICANT: GECZY, ANDREW F
TITLE OF INVENTION: T-CELL EPITOPES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K STREET, N.W.
CITY: WASHINGTON, D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 07/987,286
FILING DATE: 16-MAR-1993
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/AU91/00429
FILING DATE: 17-SEP-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PK2361
FILING DATE: 18-SEP-1990

ATTORNEY/AGENT INFORMATION:

NAME: BENT, STEPHEN A.
REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 16786/175/CHAC
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1

OTHER INFORMATION: /note= "RESIDUE 1 IS PYROGLUTAMIC

OTHER INFORMATION: ACID"

FEATURE:

NAME/KEY: Modified-site

LOCATION: 25

OTHER INFORMATION: /note= "RESIDUE 25 IS CYSTEINAMIDE"

Query Match 2.4%; Score 6; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 GAALGA 41
Db 15 GAALGA 20

RESULT 55
US-07-987-286-24
Sequence 24, Application 07/987286
Patent No. 5500366

GENERAL INFORMATION:

APPLICANT: RUSSELL-JONES, GREGORY J
APPLICANT: GECZY, ANDREW F
TITLE OF INVENTION: T-CELL EPITOPES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K STREET, N.W.
CITY: WASHINGTON, D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 07/987,286
FILING DATE: 16-MAR-1993
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/AU91/00429
FILING DATE: 17-SEP-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PK2361
FILING DATE: 18-SEP-1990

ATTORNEY/AGENT INFORMATION:

NAME: BENT, STEPHEN A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/175/CHAC
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-987-286-24

Query Match 2.4%; Score 6; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 GAALGA 41
Db 16 GAALGA 21

RESULT 56
US-08-614-626-11
Sequence 11, Application US/08614626
Patent No. 5928644

GENERAL INFORMATION:

APPLICANT: RUSSELL-JONES, GREGORY J
APPLICANT: GECZY, ANDREW F
TITLE OF INVENTION: T-CELL EPITOPES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K STREET, N.W.

CITY: WASHINGTON, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/614,626
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/987,286
FILING DATE: 16-MAR-1993
APPLICATION NUMBER: PCT/AU91/00429
FILING DATE: 17-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK2361
FILING DATE: 18-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, STEPHEN A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/175/CHAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "RESIDUE 1 IS PYROGLUTAMIC
OTHER INFORMATION: ACID"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 25
OTHER INFORMATION: /note= "RESIDUE 25 IS CYSTEINAMIDE"
US-08-614-626-11
Query Match 2.4%; Score 6; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 36 GAALGA 41
15 GAALGA 20
RESULT 57
US-08-614-626-24
Sequence 24, Application US/08614626
Patent No. 5928644
GENERAL INFORMATION:
APPLICANT: RUSSELL-JONES, GREGORY J
APPLICANT: GECZY, ANDREW P
TITLE OF INVENTION: T-CELL EPITOPES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K STREET, N.W.
CITY: WASHINGTON, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/614,626
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/987,286
FILING DATE: 16-MAR-1993
APPLICATION NUMBER: PCT/AU91/00429
FILING DATE: 17-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK2361
FILING DATE: 18-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, STEPHEN A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/175/CHAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-614-626-24
Query Match 2.4%; Score 6; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 36 GAALGA 41
16 GAALGA 21
RESULT 58
US-09-230-548-20
Sequence 20, Application US/09230548
Patent No. 6328466
GENERAL INFORMATION:
APPLICANT: Bottaro, Donald P.
APPLICANT: Petryshyn, Raymond
APPLICANT: The Government of the United States of America
APPLICANT: as represented by The Secretary,
Department of Health and Human Services
TITLE OF INVENTION: Double-stranded RNA Dependent Protein Kinase Derived
Peptides to Promote Proliferation of Cells and Tissues
FILE REFERENCE: 015280-286200US
CURRENT APPLICATION NUMBER: US/09/230,548
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: US 60/023,307
EARLIER FILING DATE: 1996-07-30
EARLIER APPLICATION NUMBER: WO PCT/US97/14350
EARLIER FILING DATE: 1997-07-29
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 25
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: double-stranded
OTHER INFORMATION: RNA dependent protein kinase (PKR) peptide
OTHER INFORMATION: antagonist, cell-membrane permeable peptide
US-09-230-548-20
Query Match 2.4%; Score 6; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 Llapkg 13
| | | | |
Db 13 Llapkg 18

RESULT 59

US-09-181-941-9
Sequence 9, Application US/09181941
Patent No. 6440690

GENERAL INFORMATION:

APPLICANT: MOR, Amram
Vouldoukis, Ioannis

Nicolas, Pierre

TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION
OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY

COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/181,941

FILING DATE: 28-Oct-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/574,701

FILING DATE: 19-DEC-1995

APPLICATION NUMBER: FR 95 07831

FILING DATE: 29-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 3909-0021-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6440690e

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-181-941-9

Query Match

Best Local Similarity 2.4%; Score 6; DB 4; Length 30;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AALGAV 42
| | | | |
Db 17 AALGAV 22

US-09-181-941-9

Query Match

Best Local Similarity 2.4%; Score 6; DB 4; Length 30;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AALGAV 42
| | | | |
Db 17 AALGAV 22

US-09-181-941-9

Query Match

Best Local Similarity 2.4%; Score 6; DB 4; Length 30;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AALGAV 42
| | | | |
Db 17 AALGAV 22

US-09-181-941-9

Query Match

Best Local Similarity 2.4%; Score 6; DB 4; Length 30;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AALGAV 42
| | | | |
Db 17 AALGAV 22

TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION
OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY

COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/181,941

FILING DATE: 28-Oct-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/574,701

FILING DATE: 19-DEC-1995

APPLICATION NUMBER: FR 95 07831

FILING DATE: 29-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 3909-0021-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6440690e

SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-181-941-14

Query Match

Best Local Similarity 2.4%; Score 6; DB 4; Length 33;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AALGAV 42
| | | | |
Db 24 AALGAV 29

US-09-369-494-16

Query Match

Best Local Similarity 2.4%; Score 6; DB 4; Length 33;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AALGAV 42
| | | | |
Db 24 AALGAV 29

US-09-369-494-16

Query Match

Best Local Similarity 2.4%; Score 6; DB 4; Length 33;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AALGAV 42
| | | | |
Db 24 AALGAV 29

US-09-369-494-16

Query Match

Best Local Similarity 2.4%; Score 6; DB 4; Length 33;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AALGAV 42
| | | | |
Db 24 AALGAV 29

US-09-369-494-16

Query Match

Best Local Similarity 2.4%; Score 6; DB 4; Length 33;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AALGAV 42
| | | | |
Db 24 AALGAV 29

US-09-369-494-16

Query Match

Best Local Similarity 2.4%; Score 6; DB 4; Length 33;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AALGAV 42
| | | | |
Db 24 AALGAV 29

US-09-369-494-16

Query Match

Best Local Similarity 2.4%; Score 6; DB 4; Length 33;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 2.4%: Score 6; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 166 YSOVL 171
|||
Db 46 YSOVL 51

RESULT 62
US-09-358-569D-14
; Sequence 14, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznak, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: from computer
; OTHER INFORMATION: database
US-09-358-569D-14

Query Match 2.4%: Score 6; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 166 YSOVL 171
|||
Db 46 YSOVL 51

RESULT 63
US-09-655-270A-30
; Sequence 30, Application US/09655270A
; Patent No. 6329151
; GENERAL INFORMATION:
; APPLICANT: Rouviere, Pierre E.
; TITLE OF INVENTION: High Density Sampling of Differentially Expressed Prokaryotic m
; FILE REFERENCE: BC1011 US NA
; CURRENT APPLICATION NUMBER: US/09/655,270A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/120,702
; PRIOR FILING DATE: 1999-February-19
; PRIOR APPLICATION NUMBER: 60/152,542
; PRIOR FILING DATE: 1999-September-03
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 30
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: microbial enrichment culture-
; OTHER INFORMATION: not one single organism
US-09-655-270A-30

Query Match 2.4%: Score 6; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 103 RRAVLT 108
|||

Db 49 RRAVLT 54

RESULT 64
US-09-247-155-112
; Sequence 112, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclet, Aymeric
; APPLICANT: Bougueret, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET.021A
; CURRENT APPLICATION NUMBER: US/09/247,155A
; CURRENT FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/074,121
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/081,563
; EARLIER FILING DATE: 1998-04-13
; EARLIER APPLICATION NUMBER: 60/096,116
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/099,273
; EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.in
; SEQ ID NO 112
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -74...-1
US-09-247-155-112

Query Match 2.4%: Score 6; DB 4; Length 86;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 SPFLA 10
|||
Db 36 SPFLA 41

RESULT 65
US-08-710-749-28
; Sequence 28, Application US/08710749
; Patent No. 5955989
; GENERAL INFORMATION:
; APPLICANT: Biles, David E.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Becker, Robert
; TITLE OF INVENTION: STRAIN SELECTION OF PNEUMOCOCCAL SURFACE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtiss, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,749
; FILING DATE: 20-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506

REFERENCE/DOCKET NUMBER: 454312-2074
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
STRANDEDNESS: n/a
TOPOLOGY: linear
MOLECULE TYPE: amino acid
US-08-710-749-28

Query Match 2.4%; Score 6; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 SONGRG 77
|||||
53 SONGEG 58

RESULT 66
US-08-469-260A-253
Sequence 253, Application US/08469260A
Patent No. 6451578
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAM J. PILOT-MATIAS
APPLICANT: GEORGE J. DAMSON
APPLICANT: GEORGE G. SCHLUEDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEHROFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAMMAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESSES:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,260A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 253:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-260A-253

Query Match 2.4%; Score 6; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 LRRGRG 147
|||||
Db 31 LRRGRG 36

RESULT 67
US-09-199-637A-353
Sequence 353, Application US/09199637A
Patent No. 6355411
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick
APPLICANT: Goodman, Howard M.
APPLICANT: Rahme, Laurence G.
APPLICANT: Mahajan-Miklos, Shalina
APPLICANT: Tan, Man-Wah
APPLICANT: Cao, Hui
APPLICANT: Drenkard, Eliana
APPLICANT: Tsengalis, John
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 00786/361002
CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/066,517
PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 353
LENGTH: 122
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-353

Query Match 2.4%; Score 6; DB 4; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 RKRRAV 106
|||||
Db 38 RKRRAV 43

RESULT 68
US-08-858-207A-490
Sequence 490, Application US/08858207A
Patent No. 6348328
GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328e1 Compounds
NUMBER OF SEQUENCES: 552
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A

FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmil, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50475
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 490:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6348328e
08-858-207A-490

Query Match 2.4%; Score 6; DB 4; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 RAVLTQ 109
DB 107 RAVLTQ 112

RESULT 69
US-09-199-637A-371
Sequence 371, Application US/09199637A
Patent No. 6355411
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick
APPLICANT: Goodman, Howard M.
APPLICANT: Rahme, Laurence G.
APPLICANT: Mahajan-Miklos, Shalina
APPLICANT: Cao, Hui
APPLICANT: Tan, Man-Wah
APPLICANT: Drenkard, Eliana
APPLICANT: Tsongalis, John
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 00786/361002
CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/066,517
PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 371
LENGTH: 129
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-371

Query Match 2.4%; Score 6; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 ALSVAL 31
DB 12 ALSVAL 17

RESULT 70
US-07-994-469A-10
Sequence 10, Application US/07994469A
Patent No. 5519119
GENERAL INFORMATION:

APPLICANT: Yamada, No. 5519119utoeshi
APPLICANT: Kato, Masanari
APPLICANT: Miyata, Keizo
APPLICANT: Aoyama, Yoshiyuki
APPLICANT: Shikama, Hiroshi
TITLE OF INVENTION: Polypeptide
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/994,469A
FILING DATE: 21-DEC-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5519119man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 72-085-0 FMC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)413-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-994-469A-10

Query Match 2.4%; Score 6; DB 1; Length 139;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 YSOVLV 171
DB 49 YSOVLV 54

RESULT 71
US-08-997-080-47
Sequence 47, Application US/08997080
Patent No. 5968524
GENERAL INFORMATION:
APPLICANT: WATSON, JAMES D.
APPLICANT: TAN, PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,080
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-997-080-47
Query Match 2.4%; Score 6; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 36 GAAIGA 41
Db 9 GAAIGA 14
RESULT 72
US-08-997-362-47
Sequence 47, Application US/08997362
Patent No. 5985287
GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Hiyma, Jun
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Scott, Linda
APPLICANT: Prestidge, Rose
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,362
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
FILING DATE: August 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-997-362-47
Query Match 2.4%; Score 6; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 36 GAAIGA 41
Db 9 GAAIGA 14
RESULT 73
US-08-873-970-47
Sequence 47, Application US/08873970
Patent No. 6001361
GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Hiyma, Jun
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Scott, Linda
APPLICANT: Prestidge, Rose
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,970
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-873-970-47
Query Match 2.4%; Score 6; DB 3; Length 142;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 36 GAAIGA 41
Db 9 GAAIGA 14

Db 9 GAALGA 14

RESULT 74
US-09-095-855-47
Sequence 47, Application US/09095855
Patent No. 6160093
GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
TITLE OF INVENTION: Compounds and Methods for
NUMBER OF SEQUENCES: 208
TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095.855
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705.347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873.970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997.362
FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-095-855-47

Query Match 2.4% Score 6; DB 4; Length 142;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 GAALGA 41
|||||
Db 9 GAALGA 14

RESULT 75
US-08-705-347A-47
Sequence 47, Application US/08705347A
Patent No. 6284255
GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Miyama, Jun
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot

APPLICANT: Scott, Linda
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Speckman Picard PLLC
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705.347A
FILING DATE: 28-AUG-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206.269.0565
TELEFAX: 206.269.0563
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-705-347A-47

Query Match 2.4% Score 6; DB 4; Length 142;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 GAALGA 41
|||||
Db 9 GAALGA 14

Search completed: March 26, 2003, 07:50:08
Job time : 37 secs

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OM protein - protein search, using sw model

Run on: March 26, 2003, 07:42:50 ; Search time 44 Seconds
(without alignments)
546.218 Million cell updates/sec

Title: us-09-724-341-8

Perfect score: 250
Sequence: 1 MPASSPFLAPKGPNGMG.....RARKLNLSPHGTFLEGVKL 250

Scoring table:

OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

d size: 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database:

PIR_73: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	3.2	327	2	AB2194
2	8	3.2	645	2	A75350
3	7	2.8	27	2	AS3727
4	7	2.8	76	2	T17719
5	7	2.8	78	2	BS4897
6	7	2.8	94	2	S44064
7	7	2.8	101	2	C69930
8	7	2.8	106	1	G1BEPR
9	7	2.8	127	2	T27873
10	7	2.8	146	2	T36476
11	7	2.8	180	2	T50598
12	7	2.8	181	2	T49759
13	7	2.8	219	2	T18797
14	7	2.8	232	1	G65197
15	7	2.8	232	2	P81233
16	7	2.8	232	2	F86080
17	7	2.8	232	2	AB0010
18	7	2.8	232	2	AC0943
19	7	2.8	252	2	F70711
20	7	2.8	255	2	AH0577
21	7	2.8	285	2	F70907
22	7	2.8	287	2	T22605
23	7	2.8	289	2	AB2054
24	7	2.8	314	2	A87629
25	7	2.8	326	2	T05674
26	7	2.8	352	1	T1BOBI
27	7	2.8	359	2	T22774
28	7	2.8	364	1	U70579
29	7	2.8	364	1	A39133

30	7	2.8	401	2	F65063	Cysteine sulfinate
31	7	2.8	401	2	F91087	hypothetical prote
32	7	2.8	401	2	H85932	hypothetical prote
33	7	2.8	421	2	AD3393	bicyclomycin resis
34	7	2.8	437	2	A72513	hypothetical prote
35	7	2.8	442	2	C87058	conserved hypotnet
36	7	2.8	470	2	G70870	hypothetical prote
37	7	2.8	473	2	G69789	sugar transporter
38	7	2.8	477	2	C42214	peroxisome prolif
39	7	2.8	488	2	F86209	protein F2265.14
40	7	2.8	492	1	P2MRB	L2 protein - cort
41	7	2.8	506	2	AF2192	bitfunctional purin
42	7	2.8	587	2	S49942	hypothetical prote
43	7	2.8	588	2	T35549	hypothetical prote
44	7	2.8	601	2	T46084	CDPK-related prote
45	7	2.8	611	2	T27013	hypothetical prote
46	7	2.8	657	2	H70872	probable ctcp prot
47	7	2.8	670	2	T00083	hypothetical prote
48	7	2.8	680	1	CGHUID	collagen alpha 1(X
49	7	2.8	705	2	T35165	probable integral
50	7	2.8	731	2	G87648	sensory box histid
51	7	2.8	771	2	F70757	probable cation tr
52	7	2.8	824	2	T44037	helicase [imported
53	7	2.8	824	2	T44222	probable helicase
54	7	2.8	860	2	C86203	hypothetical prote
55	7	2.8	1040	2	S50617	BEB1 protein - yea
56	7	2.8	1090	2	A41541	adenylate cyclase
57	7	2.8	1134	2	F87642	hypothetical prote
58	7	2.8	1245	2	H83574	conserved hypotnet
59	7	2.8	1294	2	T35044	bacteriophage phiC
60	7	2.8	1347	2	F84531	probable retroelem
61	7	2.8	1446	1	A45344	immediate-early pr
62	7	2.8	1460	1	EDBEIF	immediate-early pr
63	7	2.8	2037	2	T16881	hypothetical prote
64	7	2.8	2118	2	S72705	mycocerosate synh
65	7	2.8	2344	1	RKMWRH	mycocerosate synh
66	7	2.8	2344	2	S64740	genome polypeptid
67	7	2.8	2408	2	T24483	hypothetical prote
68	7	2.8	2629	2	T30987	telomerase-associ
69	7	2.8	2629	2	T32735	telomerase-associ
70	7	2.4	18	2	S10452	telomerase-associ
71	7	2.4	23	2	C56978	hypothetical prote
72	7	2.4	43	2	C41397	collagen alpha 1(I
73	7	2.4	55	2	A69850	hypothetical prote
74	7	2.4	63	2	C90826	hypothetical prote
75	7	2.4	71	2	C75627	hypothetical prote
76	7	2.4	74	2	T10456	hypothetical prote
77	7	2.4	77	2	T22249	dermaeapine B3 pr
78	7	2.4	78	2	T39665	ubiquitin-like pro
79	7	2.4	78	2	G86254	ubiquitin-like pro
80	7	2.4	81	1	JN0462	adenoregulin precu
81	7	2.4	81	2	JN0710	ubiquitin-like pro
82	7	2.4	88	2	T14944	hypothetical prote
83	7	2.4	88	2	A13287	hypothetical prote
84	7	2.4	99	2	B86203	hypothetical prote
85	7	2.4	100	2	AF1490	hypothetical prote
86	7	2.4	101	2	G82648	conserved hypotnet
87	7	2.4	102	2	F84709	conserved hypotnet
88	7	2.4	104	2	AH0040	probable glutaredo
89	7	2.4	104	2	AC1130	conserved hypotnet
90	7	2.4	107	2	T46583	hypothetical prote
91	7	2.4	107	2	G71517	ferredoxin [import
92	7	2.4	109	2	D47056	probable l21 ribos
93	7	2.4	111	2	C88678	car regulatory pro
94	7	2.4	111	2	E25035	protein H06421.7
95	7	2.4	114	2	B87690	colicin Ia immunit
96	7	2.4	115	2	C83574	hypothetical prote
97	7	2.4	117	2	T37543	hypothetical prote
98	7	2.4	117	2	B75344	60s ribosomal prot
99	7	2.4	118	2	D82061	conserved hypotnet
100	7	2.4	118	2	A11334	ribosomal protein

ALIGNMENTS

RESULT 1

AB2194 hypothetical protein al3105 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp.

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002

C:Accession: AB2194

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kunitz, T.; Sasamoto, S.; Matanabe, A.; Iriuchihara, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Ref: 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AB2194

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-327 <KUR>

A:Cross-references: GB:BA000019; PIDN:BA874804.1; PID:G17132199; GSPDB:GN00179

A:Experimental source: strain PCC 7120

A:Genetics:

A:Gene: al3105

Query Match 3.2%; Score 8; DB 2; Length 327;

Best Local Similarity 100.0%; Pred. No. 6;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 QSSDALEA 93

DB 162 QSSDALEA 169

RESULT 2

A75390 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 DR1494 [similarity] - Deinococcus

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Jun-2002

C:Accession: A75390

R:Wille, O.; Eisen, J.A.; Heldberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

S.; Shen, M.; Vamshaveyan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma

S.; Smith, H.O.; Venter, J.C.; Frazer, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: A75390

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-645 <WHI>

A:Cross-references: GB:AE001993; GB:AE00513; NID:G6459244; PIDN:AF11057.1; PID:G645925

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR1494

A:Map position: 1

C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5

C:Keywords: membrane-associated complex; NAD; oxidoreductase

Query Match 3.2%; Score 8; DB 2; Length 645;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 212 YSAGVFHL 219

DB 345 YSAGVFHL 352

RESULT 3

A53727 dermaseptin b - two-colored leaf frog

C:Species: Phyllomedusa bicolor (two-colored leaf frog)

C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 09-Apr-1998

C:Accession: A53727

R:Mor, A.; Amiche, M.; Nicolas, P.

Biochemistry 33, 6642-6650, 1994

A:Title: Structure, synthesis, and activity of dermaseptin b, a novel vertebrate defens

A:Reference number: A53727; MUID:94263975; PMID:8204601

A:Accession: A53727

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-27 <MOR>

C:Superfamily: dermaseptin precursor; dermorphin precursor amino-terminal homology

C:Keywords: skin

Query Match 2.8%; Score 7; DB 2; Length 27;

Best Local Similarity 100.0%; Pred. No. 6.7;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AALGAVA 43

DB 16 AALGAVA 22

RESULT 4

T17719 hypothetical protein a228R - Chlorella virus PBCV-1

C:Species: Chlorella virus PBCV-1

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T17719

R:Graves, M.V.; Van Etten, J.L.

submitted to the EMBL Data Library, May 1999

A:Reference number: Z18806

A:Accession: T17719

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-76 <GRA>

A:Cross-references: EMBL:U42580; NID:G4028896; PIDN:AAC96596.1

A:Experimental source: specific host Chlorella strain NC64A

C:Genetics:

A:Note: a228R

Query Match 2.8%; Score 7; DB 2; Length 76;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 LSVLWML 33

DB 69 LSVLWML 75

RESULT 5

B54897 dermaseptin b I precursor - two-colored leaf frog

C:Species: Phyllomedusa bicolor (two-colored leaf frog)

C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 16-Jul-1999

C:Accession: B54897

R:Amiche, M.; Ducancel, F.; Mor, A.; Boulain, J.C.; Menez, A.; Nicolas, P.

J. Biol. Chem. 269, 17847-17852, 1994

A:Title: Precursors of vertebrate peptide antibiotics dermaseptin b and adeno regulin ha

A:Reference number: A54897; MUID:94299491; PMID:8074751

A:Accession: B54897

A:Molecule type: mRNA

A:Residues: 1-78 <AMT>

A:Cross-references: GB:X72387; NID:G505483; PIDN:CAA51080.1; PID:G505484

C:Superfamily: dermaseptin precursor; dermorphin precursor amino-terminal homology

C:Keywords: amidated carboxyl end; antibiotic; antifungal; skin

F:1-44/Domain: dermorphin precursor amino-terminal homology <DER>

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-44/Domain: propeptide #status predicted <PRO>

F:49-75/Product: dermaseptin b I #status experimental <MAT>

F:75/Modified site: amidated carboxyl end (Gln) (amide in mature form from following 91

Query Match 2.8%; Score 7; DB 2; Length 78;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AALGAVA 43
|||||
Db 64 AALGAVA 70

RESULT 6

S44064

antifungal protein precursor - Aspergillus giganteus

C/Species: Aspergillus giganteus

C/Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Jul-2000

C/Accession: S44064; S13203; S10314; S21865

R/Mendt, S.; Ulbrich, N.; Stahl, U.

Curr. Gene. 25, 519-523, 1994

A/Title: Molecular cloning, sequence analysis and expression of the gene encoding an ant

A/Reference number: S44064; MUID:94363778; PMID:8082203

A/Accession: S44064

A/Molecule type: DNA

A/Residues: 194 <MNE>

A/Cross-references: EMBL:X60771; NID:92307; PIDN:CAA43181.1; PID:92308

Nakaya, K.; Omata, K.; Okahashi, I.; Nakamura, Y.; Kolkenbrock, H.; Ulbrich, N.

F. J. Biochem. 193, 31-38, 1990

A/Title: Amino acid sequence and disulfide bridges of an antifungal protein isolated fr

A/Reference number: S13203; MUID:91031461; PMID:2226447

A/Accession: S13203

A/Molecule type: protein

A/Residues: 44-94 <NAK>

R/Mendt, S.; Ulbrich, N.; Stahl, U.

Nucleic Acids Res. 18, 3987, 1990

A/Title: Cloning and nucleotide sequence of a cDNA encoding the antifungal-protein of A

A/Reference number: S10314; MUID:90326523; PMID:2374718

A/Accession: S10314

A/Molecule type: mRNA

A/Residues: 20-79 <MNM>

A/Cross-references: EMBL:X53432

C/Genetics:

A/Introns: 48/3; 75/3

C/Keywords: antifungal; disulfide bond

F/1-26/Domain: signal sequence #status predicted <SIG>

F/7-43/Domain: propeptide #status predicted <PRO>

F/44-94/Product: antifungal protein #status experimental <MAT>

F/50-76,57-83,69-71,92-94/Disulfide bonds: #status experimental

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 94;
Pred. No. 21;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AALGAVA 43
|||||

15 AALGAVA 21

RESULT 7

C69930

hypothetical protein yoxC - Bacillus subtilis

C/Species: Bacillus subtilis

C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000

C/Accession: C69930

R/Kunze, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Beret

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; C

A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A/Authors: Leiber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue

Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portelle

Rieger, M.; Rivolta, C.; Roche, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,

A/Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Ser

T.; Winters, P.; Wipit, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A/Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A/Reference number: A69580; MUID:98044033; PMID:9384377

A/Accession: C69930
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-101 <KUN>
A/Cross-references: GB:299114; GB:AL009126; NID:62634230; PIDN:CAB3744.1; PID:92634245
C/Genetics:
A/Experimental source: strain 168
C/Superfamily: Bacillus subtilis hypothetical protein yoxC

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 101;
Pred. No. 22;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 LTOKOKK 113
|||||

Db 57 LTOKOKK 63

RESULT 8

GIBEP

tegument protein - suid herpesvirus 1 (strain Rice)

C/Species: suid herpesvirus 1

C/Note: host Sus scrofa domestica (domestic pig)

C/Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 16-Jul-1999

C/Accession: A27815

R/Petrovskis, E.A.; Post, L.E.

Virology 159, 193-195, 1987

A/Title: A small open reading frame in pseudorabies virus and implications for evolutio

A/Reference number: A27815; MUID:87265472; PMID:3037781

A/Accession: A27815

A/Molecule type: DNA

A/Residues: 1-106 <PET>

A/Cross-references: GB:M16769; NID:9334041; PIDN:AAA7462.1; PID:9334042

C/Superfamily: human herpesvirus tegument protein; herpesvirus tegument protein homolog

F/48-100/Domain: herpesvirus tegument protein homology <HTP>

Query Match

Best Local Similarity 100.0%; Score 7; DB 1; Length 106;
Pred. No. 23;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLAOKGP 14
|||||

Db 30 LLAOKGP 36

RESULT 9

T27873

hypothetical protein ZK470.3 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000

C/Accession: T27873

R/Minx, P.

submitted to the EMBL Data Library, October 1995

A/Description: The sequence of C. elegans cosmid ZK470.

A/Reference number: Z20433

A/Accession: T27873

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-127 <MIN>

A/Cross-references: EMBL:U39651; PIDN:AAA80393.1; CESP:ZK470.3

C/Genetics:

A/Gene: CESP:ZK470.3

A/Introns: 17/2; 31/3; 81/1; 110/3

C/Superfamily: Caenorhabditis elegans hypothetical protein ZK470.3

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 127;
Pred. No. 27;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LOSLRRE 61
|||||

Db 109 LOSLRRE 115

RESULT 10

T36476

hypothetical protein SCF85.16 - Streptomyces coelicolor

C/Species: Streptomyces coelicolor

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C/Accession: T36476

R/Seeger, K.J.; Harris, D.; Thomson, N.R.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, September 1999

A/Reference number: Z21607

A/Accession: T36476

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-146 <SEE>

A/Cross-references: EMBL:AL110470; PIDN:CAB54173.1; GSPDB:GN00070; SCOEDB:SCF85.16

A/Experimental source: strain A3(2)

C/Genetics:

A/Gene: SCOEDB:SCF85.16

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 146;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AALGAVA 43

DB 48 AALGAVA 54

RESULT 11

T50598

probable membrane protein [imported] - Streptomyces coelicolor

C/Species: Streptomyces coelicolor

C/Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000

C/Accession: T50598

R/Redenbach, M.; Kieseer, H.M.; Denapalte, D.; Eichner, A.; Cullum, J.; Kinashi, H.; Hopx

Mol. Microbiol. 21, 77-96, 1996

A/Title: A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb S

A/Reference number: Z20556; MUID:97000351; PMID:8843436

A/Accession: T50598

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-180 <RED>

A/Cross-references: EMBL:AL133220; PIDN:CAB61735.1

A/Experimental source: strain A3(2)

C/Genetics:

A/Note: SCC75A.35

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 180;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 GROETLF 194

DB 173 GROETLF 179

RESULT 12

T49759

related to microcin e492 precursor [imported] - Neurospora crassa

N/Alternate names: protein B24B19.310

C/Species: Neurospora crassa

C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000

C/Accession: T49759

R/Schulte, U.; Aijn, V.; Hobeisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,

submitted to the Protein Sequence Database, May 2000

A/Reference number: Z25022

A/Accession: T49759

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-181 <SCH>

A/Cross-references: EMBL:AL356192; GSPDB:GN00116; NCSP:B24B19.310

A/Experimental source: BAC clone B24B19; strain OR74A

C/Genetics:
 A/Gene: NCSP:B24B19.310
 A/Map position: 6
 A/Introns: 52/3; 66/2; 126/1; 141/3

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 181;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AALGAVA 43

DB 122 AALGAVA 128

RESULT 13

T18797

hypothetical protein C01A2.6 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000

C/Accession: T18797

R/Kershaw, J.

submitted to the EMBL Data Library, October 1996

A/Reference number: Z19023

A/Accession: T18797

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-219 <WIL>

A/Cross-references: EMBL:Z81029; PIDN:CAB02701.1; GSPDB:GN00019; CESP:C01A2.6

A/Experimental source: clone C01A2

C/Genetics:

A/Gene: CESP:C01A2.6

A/Map position: 1

A/Introns: 22/1; 160/3

C/Superfamily: Caenorhabditis elegans hypothetical protein C01A2.6

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 219;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 LEAWENG 97

DB 85 LEAWENG 91

RESULT 14

C65197

transcription regulator cpxR - Escherichia coli (strain K-12)

N/Alternate names: transcription factor (cpxA 5' region)

C/Species: Escherichia coli

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002

C/Accession: C65197; S40856; I53679; S08331

R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A/Title: The complete genome sequence of Escherichia coli K-12.

A/Reference number: A64720; MUID:97426617; PMID:9278503

A/Accession: C65197

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-232 <BLAT>

A/Cross-references: GB:AE000466; GB:U00096; NID:G2367328; PIDN:AACT6894.1; PID:G2367329

A/Experimental source: strain K-12, substrain MG1655

R/Plunkett III, G.; Burland, V.; Daniels, D.L.; Blattner, F.R.

Nucleic Acids Res. 25, 3391-3398, 1997

A/Title: Analysis of the Escherichia coli genome. III. DNA sequence of the region from

A/Reference number: S40802; MUID:93347969; PMID:8346018

A/Accession: S40856

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-115 'X', 117-232 <PLU>

A/Cross-references: EMBL:U19201; NID:G304961; PIDN:AA03045.1; PID:G305016

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1993

R/Dong, J.; Iuchi, S.; Kwan, H.S.; Lu, Z.; Lin, E.C.

Gene 136, 227-230, 1993
A/Title: The deduced amino-acid sequence of the cloned cpxR gene suggests the protein is
hla coli.
A/Accession: 153679; MUID:94124003; PMID:8294007
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-232 <RES>
A/Cross-references: GB:L14579; NID:G410156; PIDN:AAC36868.1; PID:G410157
R/Weber, R.F.; Silverman, P.M.
J. Mol. Biol. 203, 467-478, 1998
A/Title: The Cpx proteins of *Escherichia coli* K12. Structure of the CpxA polypeptide as
A/Reference number: S01377; MUID:89068697; PMID:3058985
A/Accession: S08331
A/Molecule type: DNA
A/Residues: 138-232 <WEB>
A/Cross-references: EMBL:X13307; NID:G41150; PIDN:CAA31686.1; PID:G41151
C/Genetics:
A/Gene: cpxR
Superfamily: ompR protein; response regulator homology
Keywords: phosphoprotein
4-11/Domain: response regulator homology <RRH>
F/51/Binding site: phosphate (asp) (covalent) #status predicted

Query Match 2.8%; Score 7; DB 1; Length 232;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 GQVVSRE 185
DB 173 GQVVSRE 179

RESULT 15

P91233
hypothetical protein EC64838 [imported] - *Escherichia coli* (strain O157:H7, substrain R1
C/Species: *Escherichia coli*
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C/Accession: F91233
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gaenawa, N.; Yasunaga, T.; Kihara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gen
A/Reference number: A96629; MUID:21156231; PMID:11258796
A/Accession: F91233
A/Status: preliminary
A/Molecule type: DNA
Residues: 1-232 <HAY>
Cross-references: GB:BA000007; PIDN:BA838261.1; PID:G13364314; GSPDB:GN00154
Experimental source: strain O157:H7, substrain R1MD 0509952
C/Genetics:
A/Gene: EC64838
Superfamily: ompR protein; response regulator homology

Query Match 2.8%; Score 7; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 GQVVSRE 185
DB 173 GQVVSRE 179

RESULT 16

transcription regulator in 2-component system [imported] - *Escherichia coli* (strain O157
C/Species: *Escherichia coli*
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C/Accession: F86080
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dialante, E.; Potamoudis, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A/Reference number: AB5480; MUID:21074935; PMID:11206551
A/Accession: F86080
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-232 <STO>
A/Cross-references: GB:AE005174; NID:G12518811; PIDN:AAG59106.1; GSPDB:GN00145; UMGF:25
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Gene: cpxR
Superfamily: ompR protein; response regulator homology

Query Match 2.8%; Score 7; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 GQVVSRE 185
DB 173 GQVVSRE 179

RESULT 17

AB0010
two component system response regulatory protein cpxR [imported] - *Yersinia pestis* (str
C/Species: *Yersinia pestis*
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C/Accession: AB0010
R/Parhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001
A/Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360
A/Accession: AB0010
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-232 <RUR>
A/Cross-references: GB:AL590842; PIDN:CAC88940.1; PID:G15978187; GSPDB:GN00175
C/Genetics:
A/Gene: cpxR
Superfamily: ompR protein; response regulator homology

Query Match 2.8%; Score 7; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 GQVVSRE 185
DB 173 GQVVSRE 179

RESULT 18

AC0943
two-component response regulatory protein STY3812 [imported] - *Salmonella enterica* subsp.
C/Species: *Salmonella enterica* subsp. *enterica* serovar Typh
A/Note: this species has also been called *Salmonella typh*
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C/Accession: AC0943
R/Parhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher
th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A/Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* sero
A/Reference number: AB0502; PMID:11677608
A/Accession: AC0943
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-232 <PAR>
A/Cross-references: GB:AL513382; PIDN:CAM09565.1; PID:G16504679; GSPDB:GN00176
C/Genetics:
A/Gene: STY3812
Superfamily: ompR protein; response regulator homology

Query Match 2.8%; Score 7; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 179 GQVVSRE 185
|||||
Db 173 GQVVSRE 179

RESULT 19

F70711
probable membraneprotein - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C:Accession: F70711

R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sultston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: F70711

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-252 <COL>
A:Cross-references: GB:279701; GB:AL123456; NID:g3261635; PIDN:CAB02041.1; PID:g1524238

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: RV1491c

C:Superfamily: deda protein

Query Match 2.8%; Score 7; DB 2; Length 252;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 PVREPAL 27
|||||
Db 245 PVREPAL 251

RESULT 20

AH0577

mol/bdoplerin-containing oxidoreductase membrane anchor chain STY0661 [imported] - *Salmo*

C:Species: *Salmonella enterica* subsp. *enterica* serovar Typhi

A:Note: this species has also been called *Salmonella typhi*
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001

C:Accession: AH0577

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, S.; Moule, S.; O'Gaora, P.

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov

A:Reference number: AB0502; PMID:11677608

A:Accession: AH0577

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-255 <PAR>

A:Cross-references: GB:AL153382; PIDN:CAD05090.1; PID:G16501865; GSPDB:GN00176

C:Genetics:

A:Gene: STY0661

Query Match 2.8%; Score 7; DB 2; Length 255;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 203 HPDRAYN 209
|||||
Db 61 HPDRAYN 67

RESULT 21

F70907
hypothetical protein RV0587 - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C:Accession: F70907

R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sultston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: F70907

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-265 <COL>
A:Cross-references: GB:297182; GB:AL123456; NID:g3250720; PIDN:CAB09951.1; PID:g32222771

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: RV0587

C:Superfamily: conserved hypothetical protein H11086

Query Match 2.8%; Score 7; DB 2; Length 265;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 GAALGAV 42
|||||
Db 92 GAALGAV 98

RESULT 22
T22605
hypothetical protein F54B11.7 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T22605

R:Swindburne, J.

submitted to the EMBL Data Library, March 1996

A:Reference number: Z19588

A:Accession: T22605

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-287 <WIL>

A:Cross-references: EMBL:T70208; PIDN:CAA94139.1; GSPDB:GN00028; CESP:F54B11.7

C:Genetics:

A:Gene: CESP:F54B11.7

A:Map position: X

A:introns: 98/1; 209/3

Query Match 2.8%; Score 7; DB 2; Length 287;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 129 DSDSVTE 135
|||||
Db 52 DSDSVTE 58

RESULT 23
A82054
phosphoribulokinase VC2613 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)

C:Species: *Vibrio cholerae*

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C:Accession: A82054

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gilm, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, L.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the *Cholera* pathogen *Vibrio cholerae*.
A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: A82054

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-289 <HB1>
 A:Cross-references: GB:AE004328; GB:AE003852; NID:G9657201; PIDN:AAF95754.1; GSPDB:GN001
 A:Experimental source: serogroup O1, strain N16961; biotype E1 Tor
 C:Genetics:
 A:Gene: VCC613
 A:Map position: 1
 C:Superfamily: phosphoribulokinase

Query Match 2.8%; Score 7; DB 2; Length 289;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 PMQSLPE 85
 |||||
 Db 116 PMQSLPE 122

RESULT 24
 7629
 C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
 C:Accession: A87629
 R:Nierman, W.C.; Feildblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolter
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: A87629
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-314 <STO>
 A:Cross-references: GB:AE005673; NID:G13424717; PIDN:AAK25029.1; GSPDB:GN0148
 C:Genetics:
 A:Gene: CC3067

Query Match 2.8%; Score 7; DB 2; Length 314;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 LGAVACA 45
 |||||
 Db 4 LGAVACA 10

ULT 25
 5674
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 26-Aug-1999
 C:Accession: T05674
 R:Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.
 submitted to the Protein Sequence Database, February 1999
 A:Reference number: Z15420
 A:Accession: T05674
 A:Molecule type: DNA
 A:Residues: 1-326 <BEV>
 A:Cross-references: EMBL:AI035540
 A:Experimental source: cultivar Columbia; BAC clone F20M13
 C:Genetics:
 A:Map position: 4
 A:Insertions: 118/3
 A:Note: F20M13.20
 C:Superfamily: geranyltransferase

Query Match 2.8%; Score 7; DB 2; Length 326;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 ELQSLRR 60

Db 242 ELQSLRR 248
 |||||

RESULT 26
 T1BOB1
 A:Alpha-1-microglobulin / inter-alpha-trypsin inhibitor precursor [validated] - bovine
 N/Alternate names: B1-14 (inhibitory fragment of ITI); bikunin; ITI
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 25-Feb-1985 #sequence_revision 04-Feb-2000 #text_change 18-Aug-2000
 A:Accession: S68149; A91717; A90685; S31219; A01209
 R:Kindy, A.; Akers, B.
 Biochim. Biophys. Acta 1306, 98-106, 1996
 A:Title: Bovine alpha(1)-microglobulin/bikunin. Isolation and characterization of liver
 A:Reference number: S68149; MUID:96201710; PMID:8611630
 A:Accession: S68149
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-352 <LIN>
 A:Cross-references: EMBL:U35642; NID:G1016297; PIDN:AA07599.1; PID:G1016298
 R:Hochstrasser, K.; Wachter, E.
 Hoppe-Seyler's Z. Physiol. Chem. 364, 1679-1687, 1983
 A:Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-
 A:Reference number: A91717; MUID:84133807; PMID:619275
 A:Accession: A91717
 A:Molecule type: protein
 A:Residues: 227-267, 'L', 269-273, 'Q', 275-297, 'AF', 300-329, 'Q', 331-345, 'R', 347-348 <HOC>
 R:Hochstrasser, K.; Wachter, E.; Albrecht, G.J.; Reisinger, P.
 Biochem. Biophys. Res. Commun. 1985
 A:Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-
 A:Reference number: A90685; MUID:85225967; PMID:2408637
 A:Accession: A90685
 A:Molecule type: protein
 A:Residues: 347-349 <HOC2>
 R:Hochstrasser, K.; Albrecht, G.J.; Schonberger, O.L.; Wachter, E.
 Hoppe-Seyler's Z. Physiol. Chem. 364, 1689-1696, 1983
 A:Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-
 A:Reference number: A91718; MUID:84133808; PMID:619276
 A:Contents: annotation; reactive sites
 R:Castillo, G.M.; Templeton, D.M.
 FEBS Lett. 318, 292-296, 1993
 A:Title: Subunit structure of bovine ESR (extracellular-matrix stabilizing factor(8)).
 A:Reference number: S31219; MUID:93178646; PMID:7680011
 A:Accession: S31219
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 206-214, 'X', 216, 'X', 218-220 <CAS>
 C:Superfamily: protein HC; animal kunitz-type proteinase inhibitor homology; lipocalin
 C:Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
 F:35-188/Domain: lipocalin homology <LRP>
 F:231-281/Domain: animal kunitz-type proteinase inhibitor homology <BP1>
 F:287-337/Domain: animal kunitz-type proteinase inhibitor homology <BP2>
 F:241/inhibitory site: Leu (chymotrypsin, elastase) #status experimental
 F:250/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:297/inhibitory site: Arg (trypsin) #status experimental

Query Match 2.8%; Score 7; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 RRAVLQ 109
 |||||
 Db 204 RRAVLQ 210

RESULT 27
 T22774
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T22774
 R:Matheis, P.
 submitted to the EMBL Data Library, February 1996

A:Reference number: Z19614
A:Accession: T22774
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-359 <MIL>
A:Cross-references: EMBL:Z69662; PIDN:CAA93499.1; GSPDB:GN00022; CESP:F56D5.1
A:Experimental source: clone F56D5
C:Genetics:
A:Gene: CESP:F56D5.1
A:Map position: 4
A:Introns: 50/3; 88/1; 252/3
C:Superfamily: unassigned collagens

Query Match 2.8%; Score 7; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PKGPGN 17
221 PKGPGN 227

RESULT 28
JTO579
triacylglycerol lipase (EC 3.1.1.3) precursor - Pseudomonas sp.
N:Alternate names: lipase
C:Species: Pseudomonas sp.
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: JTO579; PS0202; J01227; PQ0229
R:Ilizumi, T.; Nakamura, K.; Shimada, Y.; Sugihara, A.; Tomioka, Y.; Fukase, T.
Agric. Biol. Chem. 55, 2349-2357, 1991
A:Title: Cloning, nucleotide sequencing, and expression in *Escherichia coli* of a lipase
A:Reference number: JTO579; MUID:92118328; PMID:1368739
A:Accession: JTO579
A:Molecule type: DNA
A:Residues: 1-364 <IIT>
A:Cross-references: GB:D10069; GB:D01216; NID:g216898; PIDN:BAA00960.1; PID:g216899
A:Accession: PS0202
A:Molecule type: protein
A:Residues: 45-47 <IIT>
C:Genetics:
A:Gene: lip
C:Superfamily: Pseudomonas triacylglycerol lipase
C:Keywords: carboxylic ester hydrolase
F:1.44/Domain: signal sequence #status predicted <SIG>
F:45-364/Product: triacylglycerol lipase #status predicted <MAT>

Query Match 2.8%; Score 7; DB 1; Length 364;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 40 GAVACAM 46
12 GAVACAM 18

RESULT 29
A39133
triacylglycerol lipase (EC 3.1.1.3) precursor - Pseudomonas cepacia
C:Species: Pseudomonas cepacia
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A39133
R:Jorgensen, S.; Skov, K.W.; Diderichsen, B.
J. Bacteriol. 173, 559-567, 1991
A:Title: Cloning, sequence, and expression of a lipase gene from *Pseudomonas cepacia*: 11
A:Reference number: A39133; MUID:91100343; PMID:1987151
A:Accession: A39133
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-364 <JDR>
A:Cross-references: GB:M58494
C:Superfamily: Pseudomonas triacylglycerol lipase
C:Keywords: carboxylic ester hydrolase

Query Match 2.8%; Score 7; DB 1; Length 364;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 40 GAVACAM 46
12 GAVACAM 18

RESULT 30
F5063
Cysteine sulfinate desulfinase (EC 4.4.1.-) (CSD) - *Escherichia coli* (strain K-12)
C:Species: *Escherichia coli*
C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: F5063
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of *Escherichia coli* K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: F5063
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-401 <BLAT>
A:Cross-references: GB:AE000364; GB:U00096; NID:g2367162; PIDN:AACT5852.1; PID:g1789175
A:Experimental source: strain K-12, substrain MG1655
C:Superfamily: nifs protein
C:Keywords: carbon-sulfur lyase

Query Match 2.8%; Score 7; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 158 ODAGVYL 164
17 ODAGVYL 23

RESULT 31
F91087
hypothetical protein ECs3670 [imported] - *Escherichia coli* (strain O157:H7, substrain R
C:Species: *Escherichia coli*
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: F91087
R:Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hartort, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gen
A:Reference number: A9629; MUID:21156231; PMID:11258796
A:Accession: F91087
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-401 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA837093.1; PID:g13363142; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: ECs3670
C:Superfamily: nifs protein

Query Match 2.8%; Score 7; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 158 ODAGVYL 164
17 ODAGVYL 23

RESULT 32
H85932
hypothetical protein Z4127 [imported] - *Escherichia coli* (strain O157:H7, substrain EDL
C:Species: *Escherichia coli*

C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C/Accession: H85932
R/Perma: N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoudis, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: H85932
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-401 <STO>
A/Cross-references: GB:AE005174; NID:g12517292; PIDN:AAG57924.1; GSPDB:GN00145; UMGF:241
A/Experimental source: strain O157:H7, Substrain EDL933
C/Genetics:
A/Gene: 24127
C/Superfamily: nifs protein

Query Match 2.8%; Score 7; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

158 QDAGVYL 164
|||||
Db 17 QDAGVYL 23

RESULT 33
AD3393
bicyclomycin resistance protein [imported] - *Brucella melitensis* (strain 16M)
C/Species: *Brucella melitensis*
C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
C/Accession: AD3393
R/Perma: V.G.; Kapacir, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
R.; DelVecchio, V.G.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A/Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
A/Reference number: AD3252; PMID:11756688
A/Accession: AD3393
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-421 <KUR>
A/Cross-references: GB:AE008917; PIDN:ALU52311.1; PID:g17983103; GSPDB:GN00190
A/Experimental source: strain 16M
C/Genetics:
A/Gene: BME1130
A/Map position: 1
C/Superfamily: bicyclomycin resistance protein

Query Match 2.8%; Score 7; DB 2; Length 421;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

36 GAALGAV 42
|||||
Db 368 GAALGAV 374

RESULT 34
A72513
hypothetical protein APE2078 - *Aeropyrum pernix* (strain K1)
C/Species: *Aeropyrum pernix*
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C/Accession: A72513
R/Perma: Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hatakawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, *Aeropyr
A/Reference number: A72450; MUID:99310339; PMID:10382966
A/Accession: A72513
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-437 <KAW>
A/Cross-references: DDBJ:AP000063; NID:g5105654; PIDN:BAA81089.1; PID:g5105777*

A/Experimental source: strain K1
C/Genetics:
A/Gene: APE2078
C/Superfamily: conserved hypothetical protein MTH1394

Query Match 2.8%; Score 7; DB 2; Length 437;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

227 VIIPRAR 233
|||||
Db 381 VIIPRAR 387

RESULT 35
C87058
conserved hypothetical protein ML1193 [imported] - *Mycobacterium leprae*
C/Species: *Mycobacterium leprae*
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C/Accession: C87058
R/Perma: S.T.; Eigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; H
R.; Davies, R.M.; Devlin, K.; Duchoy, S.; Felwell, T.; Fraser, A.; Hamlin, N.; Holroyd
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A/Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S
A/Title: Massive gene decay in the leprosy bacillus.
A/Reference number: A86909; MUID:21128732; PMID:11234002
A/Accession: C87058
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-442 <STO>
A/Cross-references: GB:AL450380; NID:g13093158; PIDN:CAC31574.1; GSPDB:GN00147
C/Genetics:
A/Gene: ML1193

Query Match 2.8%; Score 7; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

229 IPRARAK 235
|||||
Db 306 IPRARAK 312

RESULT 36
G70870
hypothetical protein RV2522c - *Mycobacterium tuberculosis* (strain H37RV)
C/Species: *Mycobacterium tuberculosis*
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C/Accession: G70870
R/Perma: S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,
i Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A/Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A/Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
A/Reference number: A70500; MUID:98295987; PMID:9634230
A/Accession: G70870
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-470 <COL>
A/Cross-references: GB:AL021185; GB:AL123456; NID:g3261504; PIDN:CAA16018.1; PID:el2374
A/Experimental source: strain H37RV
C/Genetics:
A/Gene: RV2522c

Query Match 2.8%; Score 7; DB 2; Length 470;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

229 IPRARAK 235
|||||
Db 325 IPRARAK 331

RESULT 37

G69789

sugar transporter homolog ydjk - *Bacillus subtilis*C/Species: *Bacillus subtilis*

C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000

C/Accession: G69789

R/Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bartel, C.; Bron, S.; Bröhl, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho, A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabre, C.; Ferrari, E. Nature 390, 249-256, 1997

A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gallier, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holstappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Königstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Meneel, Y.; M.; Ogawa, K.; Ogawa, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Poterelle, R.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A.; Authors: Schlögl, S.; Schöner, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot, A.; Authors: Schuch, M.; Tamakoshi, A.; Tanaka, T.; Terpiltra, P.; Togomi, A.; Tosato, V.; Uchiyama, K.; Winere, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A/Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.

A/Reference number: A69580; MUID:98044033; PMID:9384377

A/Accession: G69789

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-473 <KUN>

A/Cross-references: GB:259107; GB:AL009126; NID:92632866; PIDN:CAB12442.1; PID:92632936

A/Experimental source: strain 168

C/Genetics:

A/Gene: ydjk

C/Superfamily: glucose transport protein

Query Match

Best Local Similarity 2.8%; Score 7; DB 2; Length 473;

Matches 7; Conservative 100.0%; Pred. No. 87;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 62 GALTAV 42

| | | | |

RESULT 38

C42214

peroxisome proliferator-activated receptor gamma chain - African clawed frog

N/Alternate names: PPAR-gamma

C/Species: *Xenopus laevis* (African clawed frog)

C/Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Sep-1999

C/Accession: C42214

R/Dreyer, C.; Krey, G.; Keller, H.; Givel, F.; Helftenbein, G.; Wahl, W. Cell 68, 879-887, 1992

A/Title: Control of the peroxisomal beta-oxidation pathway by a novel family of nuclear

A/Reference number: A42214; MUID:92191267; PMID:1313391

A/Accession: C42214

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: nucleic acid

A/Residues: 1-477 <DRE>

A/Cross-references: GB:M4163; NID:9214667; PIDN:AAA49937.1; PID:9214668

A/Note: sequence extracted from NCBI backbone (NCBI:88295)

C/Superfamily: unassigned erda-related proteins; erda transforming protein homology

C/Keywords: DNA binding; transcription regulation; zinc finger

P/111-399/Domain: erda transforming protein homology <ERBA>

Query Match

Best Local Similarity 2.8%; Score 7; DB 2; Length 477;

Matches 7; Conservative 100.0%; Pred. No. 88;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 25 PALVAL 31

| | | | |

DB 283 PALVAL 289

RESULT 39

F86209

protein P22G5.14 [imported] - *Arabidopsis thaliana*C/Species: *Arabidopsis thaliana* (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C/Accession: F86209

R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alonso, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.; Li, U.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzalli, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.

A/Reference number: A86141; MUID:21016719; PMID:11130712

A/Accession: F86209

A/Status: preliminary

A/Molecule type: DNA

A/Cross-references: GB:AE005172; NID:98778543; PIDN:AAF79551.1; GSPDB:GN00141

C/Genetics:

A/Gene: P22G5.14

A/Map position: 1

RESULT 40

P22LRB

L2 protein - cottontail rabbit papillomavirus

C/Species: cottontail rabbit papillomavirus

C/Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 24-Feb-1994

C/Accession: A03652

R/Giri, I.; Danos, O.; Yaniv, M. Proc. Natl. Acad. Sci. U.S.A. 82, 1580-1584, 1985

A/Title: Genomic structure of the cottontail rabbit (Shope) papillomavirus.

A/Reference number: A94027; MUID:85166175; PMID:2984661

A/Accession: A03652

A/Molecule type: DNA

A/Residues: 1-492 <GIR>

A/Superfamily: papillomavirus L2 protein

C/Keywords: late protein

Query Match

Best Local Similarity 2.8%; Score 7; DB 1; Length 492;

Matches 7; Conservative 100.0%; Pred. No. 91;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 99 RSRKRA 105

| | | | |

RESULT 41

AF2192

bifunctional purine biosynthesis protein [imported] - *Nostoc* sp. (strain PCC 7120)C/Species: *Nostoc* sp.A/Note: Nostoc sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002

C/Accession: AF2192

R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuch Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, DNA Res. 8, 205-213, 2001

A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *An*

A/Reference number: AB1807; MUID:21595285; PMID:11759640

A/Accession: AF2192

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-506 <KUR>
A;Cross-references: GB:BA000019; PIDN:BA874792.1; PID:G17132187; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: purH
C;Superfamily: purH bifunctional enzyme

Query Match 2.8%; Score 7; DB 2; Length 506;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 53 TELQSLR 59
Db 203 TELQSLR 209

RESULT 42
9942
hypotheical protein Y11036w - Yeast (Saccharomyces cerevisiae)
C;Alternate names: hypotheical protein Y19905.12
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence_revision 20-Feb-1995 #text_change 19-Apr-2002
C;Accession: S49942
R;Ocell, C.; Bowman, S.
Submitted to the EMBL Data Library, December 1994
A;Reference number: S49931
A;Accession: S49942
A;Molecule type: DNA
A;Residues: 1-587 <ODE>
A;Cross-references: GB:247047; EMBL:246861; NID:G603997; PID:G763310; GSPDB:GN00009; MIF
C;Genetics:
A;Gene: SGD:CST6; MIPS:Y11036w
A;Cross-references: SGD:S0001298
A;Map position: 9L
C;Superfamily: fos/jun DNA-binding domain homology
F;420-460/Domain: fos/jun DNA-binding domain homology <FUD>

Query Match 2.8%; Score 7; DB 2; Length 587;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 130 DSDYTEV 136
Db 530 DSDYTEV 536

RESULT 43
5549
hypotheical protein SC6G3.05 - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C;Accession: T35549
R;Seeger, K.U.; Harris, D.; James, K.D.; Parkhill, J.; Barrett, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, July 1999
A;Reference number: Z21582
A;Accession: T35549
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-588 <SEE>
A;Cross-references: EMBL:AL096825; PIDN:CAB46977.1; GSPDB:GN00070; SC6DB:SC6G3.05
C;Genetics:
A;Gene: SC6DB:SC6G3.05

Query Match 2.8%; Score 7; DB 2; Length 588;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 37 AALGAVA 43
Db 538 AALGAVA 544

RESULT 44
T46084
CDPK-related protein kinase - Arabidopsis thaliana
N;Alternate names: protein T20E23.130
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Mar-2000
C;Accession: T46084
R;Barques, M.; Perez-Perez, A.; Terol, J.; Torres, A.; Perez-Alonso, M.; Mewes, H.W.; L
Submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23020
A;Accession: T46084
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-601 <BAR>
A;Cross-references: EMBL:AL133363
A;Experimental source: cultivar Columbia; BAC clone T20E23
C;Genetics:
A;Map position: 3
A;Intons: 166/3; 230/2; 244/2; 280/3; 307/1; 406/1; 443/3; 479/3; 500/3; 556/3
A;Note: T20E23.130
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol

Query Match 2.8%; Score 7; DB 2; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 244 FLGFVKL 250
Db 583 FLGFVKL 589

RESULT 45
T27013
hypotheical protein Y48E1B.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T27013
R;McMurray, A.
Submitted to the EMBL Data Library, March 1997
A;Reference number: Z20299
A;Accession: T27013
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-611 <WIL>
A;Cross-references: EMBL:Z93393; PIDN:CAB07690.1; GSPDB:GN00020; CESP:Y48E1B.4
A;Experimental source: clone Y48E1B
C;Genetics:
A;Gene: CESP:Y48E1B.4
A;Map position: 2
A;Intons: 59/2; 80/3; 144/3; 413/3
C;Superfamily: Caenorhabditis elegans hypotheical protein Y48E1B.4

Query Match 2.8%; Score 7; DB 2; Length 611;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 62 VSRLOGT 68
Db 355 VSRLOGT 361

RESULT 46
H70872
probable ctcpd protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: H70872
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998

A:Authors: Sgares, R.; Suleston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987; PMID:9634230
 A:Accession: H70872
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-657 <COL>
 A:Cross-references: GB:AL021184; GB:AL123456; NID:G3261498; PIDN:CAA15997.1; PID:G279140
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: cypD
 C:Superfamily: Enterococcus copper-transferring ATPase COB; ATPase nucleotide-binding
 F:25-39/Domain: ATPase transduction domain homology <ATP>
 F:465-608/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match 2.8%; Score 7; DB 2; Length 657;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

33 LSMGAL 39
 |||||
 26 LSMGAL 32

RESULT 47
 T00083
 hypochetrical protein KIA0515 - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
 C:Accession: T00083
 R:Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.
 DNA Res. 5, 31-39, 1998
 A:Title: Prediction of the coding sequences of unidentified human genes. IX. The complete
 A:Reference number: Z14086; MUID:98290545; PMID:9628581
 A:Accession: T00083
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-670 <NAG>
 A:Cross-references: EMBL:AB011087; NID:G3043553; PIDN:BAA25441.1; PID:G3043554
 A:Experimental source: brain; clone H00183
 C:Genetics:
 A:Note: KIA0515

Query Match 2.8%; Score 7; DB 2; Length 670;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

82 SLPEOSS 88
 |||||
 309 SLPEOSS 315

RESULT 48
 CGHUIID
 collagen alpha 1(X) chain precursor - human
 N:Alternate names: procollagen alpha 1(X) chain
 C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 22-Jun-1999
 R:Reichenberger, E.; Beier, F.; Luvallie, P.; Olsen, B.R.; von der Mark, K.; Bertling, W.
 FEBS Lett. 311, 305-310, 1992
 A:Title: Genomic organization and full-length cDNA sequence of human collagen X.
 A:Reference number: S26396; MUID:93012005; PMID:1397333
 A:Accession: S26396
 A:Molecule type: DNA
 A:Residues: 1-680 <REI>
 A:Cross-references: EMBL:X68952; EMBL:X72578; EMBL:X72579; EMBL:X72580; GB:S47714; GB:S4
 R:Apde, S.S.
 submitted to the EMBL Data Library, March 1992
 A:Reference number: S30085
 A:Accession: S30086
 A:Molecule type: DNA
 A:Residues: 'TIPYGVWCWCLT', 52-680 <APT>

A:Cross-references: EMBL:X65120; NID:G23129
 A:Note: the initial difference is probably due to translation of an intronic sequence
 R:Apde, S.; Mattei, M.G.; Olsen, B.R.
 FEBS Lett. 282, 393-396, 1991
 A:Title: Cloning of human alpha-1(X) collagen DNA and localization of the COL10A1 gene
 A:Reference number: S15826; MUID:91243838; PMID:2037056
 A:Accession: S15826
 A:Molecule type: DNA
 A:Residues: 561-647, 'G', 649-666 <AP2>
 A:Cross-references: EMBL:X58879; NID:G30013; PIDN:CAA1686.1; PID:G30014
 R:Thomas, J.T.; Cresswell, C.J.; Rash, B.; Nicolai, H.; Jones, T.; Solomon, E.; Grant, I.
 Biochem. J. 280, 617-623, 1991
 A:Title: The human collagen X gene. Complete primary translated sequence and chromosoma
 A:Reference number: S18249; MUID:92109659; PMID:1764025
 A:Accession: S18249
 A:Molecule type: DNA

A:Residues: 1-26, 'T', 28-680 <THO>
 A:Cross-references: EMBL:X60382; NID:G30094; PIDN:CAA4293.1; PID:G30095
 A:Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 532-Al
 R:Reichenberger, E.; Aligner, T.; von der Mark, K.; Stoss, H.; Bertling, W.
 Dev. Biol. 148, 562-572, 1991
 A:Title: In situ hybridization studies on the expression of type X collagen in fetal hu
 A:Reference number: A43901; MUID:92077285; PMID:1743401
 A:Accession: A43901
 A:Molecule type: mRNA
 A:Residues: 547-656 <RE2>
 A:Cross-references: GB:W74050; GB:D57494; NID:G339884; PIDN:AAA61221.1; PID:G553796
 A:Note: sequence extracted from NCBI backbone (NCBI:69012, NCBI:69014)
 R:Wallis, G.A.; Rash, B.; Sweetman, W.A.; Thomas, J.T.; Super, M.; Evans, G.; Grant, M.
 Am. J. Hum. Genet. 54, 169-178, 1994
 A:Title: Amino acid substitutions of conserved residues in the carboxyl-terminal domain
 A:Reference number: IS1870; MUID:94136476; PMID:8304336
 A:Accession: IS1870

A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 520-597, 'D', 599-680 <WAL>
 A:Cross-references: GB:S68531; NID:G545180; PIDN:AAC60615.1; PID:G545181
 A:Note: mutant sequence from patient with metaphyseal chondrodysplasia type Schmid
 A:Note: a second mutant sequence with 614-Pro is also described
 C:Comment: Prolines and lysines at the third position of the tripeptide repeating unit
 ed and subsequently O-glycosylated.
 C:Genetics:
 A:Gene: GDB:COL10A1
 A:Cross-references: GDB:128635; OMIM:120110
 A:Map position: 6q21-6q22
 A:Introns: 52/1
 A:Note: a defect in this gene may cause Schmid metaphyseal chondrodysplasia
 C:Complex: type X collagen may be a homotrimer
 C:Function:
 A:Description: structural component of extracellular fibrous polymer specifically and t
 be important for skeletogenesis
 C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
 C:Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer; hydroxylysine;
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-680/Product: collagen alpha 1(X) chain #status predicted <MAT>
 F:19-56/Domain: amino-terminal nonhelical #status predicted <NCT>
 F:57-519/Region: interrupted helical
 F:550-680/Domain: amino-terminal nonhelical #status predicted <NCT>
 F:553-679/Domain: complement C1q carboxyl-terminal homology <C1Q>
 F:617/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 2.8%; Score 7; DB 1; Length 680;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GPPGNG 19
 |||||
 DB 338 GPPGNG 344

RESULT 49
 T35165

probable integral membrane protein - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999

C:Accession: J35165

R:Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

Submitted to the EMBL Data Library, July 1998

A:Reference number: Z21570

A:Accession: J35165

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-705 <SEE>

A:Cross-references: EMBL:AL031107; PDB:CA19945.1; GSPDB:GN00070; SCODEB:SC5A7.16C

A:Experimental source: strain A3(2)

C:Genetics:

Query Match 2.8%; Score 7; DB 2; Length 705;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

36 GALGAV 42
|||||
DB 537 GALGAV 543

RESULT 50

G87648
sensory box histidine kinase/response regulator (imported) - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C:Accession: G87648

R:Niernan, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Heidelberg, J.

N.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolton

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: G87648

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-731 <STO>

A:Cross-references: GB:AE005673; NID:G13424907; PDB:AAK2187.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC3225

Query Match 2.8%; Score 7; DB 2; Length 731;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

169 VLFQDVT 175
|||||
DB 311 VLFQDVT 317

RESULT 51

P70757
probable cation transport ATPase - Mycobacterium tuberculosis (strain H37Rv)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C:Accession: F70757

R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Sqare, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: F70757

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-771 <COL>

A:Cross-references: GB:Z74025; GB:AL123456; NID:G3261586; PDB:CA98411.1; PID:G3261588

A:Experimental source: strain H37Rv

C:Genetics:
A:Gene: ctpG
C:Superfamily: Enterococcus copper-transporting ATPase ctpB; ATPase nucleotide-binding
F:167-507/Domain: ATPase nucleotide-binding domain homology <ATT>
F:575-717/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match 2.8%; Score 7; DB 2; Length 771;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 ALGAVA 43
|||||
DB 218 ALGAVA 224

RESULT 52

T44037
helicase (imported) - human herpesvirus 6 (strain HST)

C:Species: human herpesvirus 6

A:Variety: strain HST

C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000

C:Accession: T44037

R:Isegawa, Y.; Mukai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.; Kaw

J.; Virol. 73, 8053-8063, 1999

A:Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A and

A:Reference number: Z22732; MUID:99412319; PMID:10482554

A:Accession: T44037

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-824 <JSE>

A:Cross-references: EMBL:AB021506; NID:G4995977; PDB:BAA78298.1; PID:G4996065

A:Experimental source: strain HST; pop. variant B

C:Genetics:

A:Note: U77

C:Superfamily: varicella-zoster virus gene 55 protein

Query Match 2.8%; Score 7; DB 2; Length 824;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ALGAVAC 44
|||||
DB 186 ALGAVAC 192

RESULT 53

T44222
probable helicase (EC 3.6.1.-) U77 [similarity] - human herpesvirus 6 (strain Z29)

C:Species: human herpesvirus 6

A:Variety: strain Z29

C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 05-May-2000

C:Accession: T44222

R:Dominguez, G.; Dambaug, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett, P.E.

J. Virol. 73, 8040-8052, 1999

A:Title: Human herpesvirus 6B genome sequence: coding content and comparison with human

A:Reference number: Z22734; MUID:99412318; PMID:10482553

A:Accession: T44222

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-824 <DOM>

A:Cross-references: EMBL:AF157706; PDB:AB06360.1

A:Experimental source: strain Z29; variant B

C:Genetics:

A:Note: U77

C:Superfamily: varicella-zoster virus gene 55 protein

C:Keywords: hydrolase

Query Match 2.8%; Score 7; DB 2; Length 824;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 ALGAVAC 44
|||||

Db 186 ALGAVAC 192

RESULT 54

C86203 hypothetical protein (imported) - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C/Accession: C86203

R/Theologian: A.; Becker, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alonso,

Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Hutzar, L.

Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maltli, R.; Marzalli,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A/Reference number: A86141; MUID:21016719; PMID:11130712

C/Accession: C86203

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-860 <STO>

A/Cross-references: GB:AEO05172; NID:G7523712; PIDN:AAE63151.1; GSPDB:GN00141

C/Genetics:

A/Map position: 1

Query Match 2.8%; Score 7; DB 2; Length 860;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 190 QETLFC 196

Db 558 QETLFC 564

RESULT 55

S50617 BEB1 protein - Yeast (Saccharomyces cerevisiae)

C/Species: Saccharomyces cerevisiae

C/Date: 28-Jan-1995 #sequence_revision 12-May-1995 #text_change 20-Jun-2000

C/Accession: S50617; S48300

R/Dietrich, F.S.

submitted to the EMBL Data Library, December 1994

A/Description: The sequence of S. cerevisiae cosmid 9781, 8198, 9115, 9981, and lambda

A/Reference number: S50617

A/Accession: S50617

A/Molecule type: DNA

A/Residues: 1-1040 <DIE>

A/Cross-references: EMBL:U18916; NID:G1384128; PIDN:AAE03212.1; PID:G603353; MIPS:YER114

R/Matsu, Y.; Matsui, R.; Toh-e, A.

submitted to the EMBL Data Library, September 1994

A/Description: The yeast gene BEB1, encoding a protein that binds Bem1p, is involved in

A/Reference number: S48300

A/Accession: S48300

A/Molecule type: DNA

A/Residues: 1-732, 'A', 734-1040 <MAT>

A/Cross-references: EMBL:D38310; NID:G550094; PIDN:BA07427.1; PID:G550095

C/Genetics:

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A/Cross-references: GB:AEO0550; NID:G202751; PIDN:AAA0682.1; PID:G202752

C/Accession: A41541

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1090 <DIE>

A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: H83574
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1245 <STO>
A:Cross-references: GB:AE004493; GB:AE004091; NID:99946436; PIDN:AG03964.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0575

Query Match 2.8%; Score 7; DB 2; Length 1245;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 LRREVS 64
Db 293 LRREVS 299

RESULT 59

Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 01-Dec-2000
C:Accession: T35044; T30203
R:Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, August 1998
A:Reference number: 221566
A:Accession: T35044
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1294 <SEE>
A:Cross-references: EMBL:AL031171; PIDN:CAA20546.1; GSPDB:GN00070; SCOREDB:SC4G2.09
A:Experimental source: strain A3(2)
J:Bedford, D.J.; Laty, C.; Burtner, M.J.
R:Bedford, D.J.; Laty, C.; Burtner, M.J.
A:Title: Two genes involved in the phase-variable phi C31 resistance mechanism of Strept
A:Reference number: 220777; MUID:95370146; PMID:7642495
A:Accession: T30203
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-372; 'N', 374-913, 'I', 915-1002, 'A', 1004-1294 <BED>
A:Cross-references: EMBL:L37531; NID:9576537; PID:9576538; PIDN:AAB00365.1
C:Genetics:
A:Gene: pgly; SCOREDB:SC4G2.09

Query Match 2.8%; Score 7; DB 2; Length 1294;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 PALRRGR 146
Db 1040 PALRRGR 1046

RESULT 60

Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: F84531
R:Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon, L.;
eueb, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402: 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: F84531
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1347 <STO>
A:Cross-references: GB:AE002093; NID:94335731; PIDN:ADD17409.1; GSPDB:GN00139
C:Genetics:

A:Gene: A2915650
A:Map position: 2
C:Superfamily: retrovirus-related polypeptide

Query Match 2.8%; Score 7; DB 2; Length 1347;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 LQSLRRE 61
Db 115 LQSLRRE 121

RESULT 61

Species: suid herpesvirus 1 (strain Kaplan)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C:Accession: A45344
R:Vicek, C.; Kozmik, Z.; Paces, V.; Schlrm, S.; Schwyzer, M.
Virology 179, 365-377, 1990
A:Title: Pseudorabies virus immediate-early gene overlaps with an oppositely oriented o
A:Reference number: A45344; MUID:91021039; PMID:2171211
A:Accession: A45344
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-1446 <VLC>
A:Cross-references: GB:M34651; NID:9334070; PIDN:AA47470.1; PID:9334071
C:Superfamily: herpesvirus immediate-early protein IE175
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 2.8%; Score 7; DB 1; Length 1446;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 ALRRGRG 147
Db 339 ALRRGRG 345

RESULT 62

Species: suid herpesvirus 1 (strain Indiana-Funkhauser)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-Feb-1997
C:Accession: S04713
R:Cheung, A.K.
Nucleic Acids Res. 17, 4637-4646, 1989
A:Title: DNA nucleotide sequence analysis of the immediate-early gene of pseudorabies v
A:Reference number: S04713; MUID:89315207; PMID:2546124
A:Accession: S04713
A:Molecule type: DNA
A:Residues: 1-1460 <CHE>
C:Superfamily: herpesvirus immediate-early protein IE175
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 2.8%; Score 7; DB 1; Length 1460;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 ALRRGRG 147
Db 347 ALRRGRG 353

RESULT 63

Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16881
R:Milcox, L.
Submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid T14G12.
 A:Reference number: Z18596
 A:Accession: T16881
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-2037 <WIL>
 A:Cross-references: EMBL:U41268; NID:G1086843; PID:G1086848; PIDN:AAA2437.1; CESP:T14G12
 C:Genetics:
 A:Gene: CESP:T14G12.5
 A:Introns: 715/2; 1484/2

Query Match 2.8%; Score 7; DB 2; Length 2037;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASSPFL 9
 DB 1060 ASSPFL 1066

RESULT 64

mycocerosate synthase (EC 2.3.1.111) - Mycobacterium leprae
 N:Alternate names: Lepb1170_C2_209 protein
 C:Species: Mycobacterium leprae
 C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 26-May-2000
 C:Accession: S72705
 R:Smith, D.R.; Robison, K.
 Submitted to the EMBL Data Library, November 1993
 A:Description: Mycobacterium leprae cosmid B1170.
 A:Reference number: S72693
 A:Accession: S72705
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-2118 <SMI>
 A:Cross-references: EMBL:U00010; NID:G466780; PIDN:AAA17069.1; PID:G466793
 C:Genetics:
 A:Start codon: TTG
 A:Superfamily: mycocerosic acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I hcnase homology; [acyl-carrier-protein] S-malonyltransferase homology
 C:Keywords: acyltransferase; carrier protein; coenzyme A
 F:28-426/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>
 F:536-816/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
 F:1449-1738/Domain: long-chain alcohol dehydrogenase homology <LADH>
 F:1770-1954/Domain: short-chain alcohol dehydrogenase homology <SADH>
 F:2038-2110/Domain: acyl carrier protein homology <ACP>

Query Match 2.8%; Score 7; DB 2; Length 2118;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 PALRRGR 146
 DB 1294 PALRRGR 1300

RESULT 65

RRWRRH
 genome polyprotein - rabbit hemorrhagic disease virus
 N:Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
 C:Species: rabbit hemorrhagic disease virus
 C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 29-May-1998
 C:Accession: A41039
 R:Meyers, G.; Wirllich, C.; Thiel, H.J.
 Virology 184, 664-676, 1991
 A:Title: Rabbit hemorrhagic disease virus--molecular cloning and nucleotide sequencing
 A:Reference number: A41039; MUID:91361557; PMID:1840711
 A:Accession: A41039
 A:Molecule type: genomic RNA
 A:Residues: 1-2344 <MEV>
 A:Cross-references: GB:M67473
 C:Superfamily: rabbit calicivirus RNA-directed RNA polymerase
 C:Keywords: nucleotidyltransferase

Query Match 2.8%; Score 7; DB 1; Length 2344;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AALGAVA 43
 DB 982 AALGAVA 988

RESULT 66

S64740
 genome polyprotein - rabbit hemorrhagic disease virus (isolate AST/89)
 N:Contains: VP60 protein
 C:Species: rabbit hemorrhagic disease virus
 A:Variety: isolate AST/89
 C:Date: 12-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Jun-2000
 C:Accession: S64740; S46944; S49018; S65012
 R:Casais, R.; Martin-Alonso, J.; Boga, J.; Parra, F.
 Submitted to the EMBL Data Library, May 1995
 A:Description: Genomic organization of rabbit hemorrhagic disease virus determined by d
 A:Reference number: S64740
 A:Accession: S64740
 A:Molecule type: genomic RNA
 A:Residues: 1-2344 <OAS>
 A:Cross-references: EMBL:Z49271; NID:G1182032; PIDN:CAA89265.1; PID:G1150552
 A:Experimental source: isolate AST/89
 R:Boga, J.; Casais, R.; Martin, M.; Martin-Alonso, J.; Carmenes, R.; Prieto, M.; Parra, F.
 Submitted to the EMBL Data Library, July 1993
 A:Description: Molecular cloning, sequence and expression of the capsid protein gene fr
 A:Reference number: S46944
 A:Accession: S46944
 A:Molecule type: genomic RNA
 A:Residues: 1650-2344 <BOG>
 A:Cross-references: EMBL:Z24757; NID:G515622; PIDN:CAA80861.1; PID:G515623
 A:Experimental source: isolate AST/89
 R:Parra, F.; Boga, J.A.; Martin, M.S.; Casais, R.
 Virology Res. 27, 219-228, 1993
 A:Title: The amino terminal sequence of VP60 from rabbit hemorrhagic disease virus supp
 A:Reference number: S49018; MUID:93255896; PMID:8488721
 A:Accession: S49018
 A:Molecule type: genomic RNA
 A:Residues: 1650-1796 <PAR>
 A:Cross-references: EMBL:Z24757
 A:Experimental source: isolate AST/89
 A:Accession: S65012
 A:Molecule type: protein
 A:Residues: 1767-1779;1875-1877,'X',1879-1881;1936-1938,'X',1940-1941 <PAW>
 C:Superfamily: rabbit calicivirus RNA-directed RNA polymerase
 C:Keywords: blocked amino end; polypeptide

Query Match 2.8%; Score 7; DB 2; Length 2344;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 AALGAVA 43
 DB 982 AALGAVA 988

RESULT 67

T24483
 hypoheterical protein T05A1.4 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
 C:Accession: T24483
 R:Lloyd, C.
 Submitted to the EMBL Data Library, December 1995
 A:Reference number: Z19897
 A:Accession: T24483
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-2408 <WIL>

A:Cross-references: EMBL:Z66219; PIDN:CAA92477.1; GSPDB:GN00022; CESP:T05A1.4
A:Experimental source: clone T05A1
C:Genetics:
A:Gene: CESP:T05A1.4
A:Map position: 4
A:Insertions: 817/1; 1320/2; 1598/1; 1879/3
C:Superfamily: Caenorhabditis elegans hypothetical protein ZK228.2

Query Match
Best Local Similarity 2.8%; Score 7; DB 2; Length 2408;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASSPFL 9
Db 1329 ASSPFL 1335

RESULT 68
T30987

telomerase-associated protein 1 - mouse
Species: Mus musculus (house mouse)

Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999

C:Accession: T30987

R:Harrington, L.; McNeil, T.; Mar, V.; Zhou, W.; Oulcon, R.; Baas, M.B.; Arruda, I.; R
Science 275, 973-977, 1997

A:Title: A mammalian telomerase-associated protein.

A:Reference number: 220952; MUID:9172559; PMID:9020079

A:Accession: T30987

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-2629 <HAR>

A:Cross-references: EMBL:U06137; NID:91835783; PID:91835784; PIDN:AAC53043.1

Query Match
Best Local Similarity 2.8%; Score 7; DB 2; Length 2629;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 PALSVAL 31
Db 1936 PALSVAL 1942

RESULT 69
T32735

telomerase-associated protein component 1 - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000

A:Accession: T32735

A:Title: T32735; a gene encoding a protein component of mammalian telomerase is a novel me

A:Residues: 1-88; 875-884, 1997

A:Reference number: 221217; MUID:97236507; PMID:9118230

A:Accession: T32735

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-2629 <NAK>

A:Cross-references: EMBL:U09282; NID:91932816; PID:91932817; PIDN:AAB51690.1

A:Experimental source: strain Fischer 344

C:Genetics:

A:Gene: T32735

C:Function:

A:Description: modification of telomerase-associated protein component 1 may regulate te

Query Match
Best Local Similarity 2.8%; Score 7; DB 2; Length 2629;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 PALSVAL 31
Db 1940 PALSVAL 1946

RESULT 70

S10452
hypothetical protein (bpha 5' region) - Aspergillus niger

C:Species: Aspergillus niger

C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Sep-1997

C:Accession: S10452

R:van Gorcom, R.F.M.; Boschloo, J.G.; Klijnenhoven, A.; Lange, J.; Bos, C.J.; van Balke

submitted to the EMBL Data Library, March 1990

A:Reference number: S10452

A:Accession: S10452

A:Molecule type: DNA

A:Residues: 1-18 <VAN>

A:Cross-references: EMBL:X52521; NID:92336; PID:92337

Query Match
Best Local Similarity 2.4%; Score 6; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 189 ROETLF 194
Db 8 ROETLF 13

RESULT 71
C56978

collagen alpha 1(I) chain - bovine (fragment)

N:Alternate names: collagen alpha 3(XI) chain

C:Species: Bos primigenius taurus (cattle)

C>Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Dec-1998

C:Accession: C56978

R:Wu, J.U.; Eyre, D.R.

J. Biol. Chem. 270, 18665-18670, 1995

A:Title: Structural analysis of cross-linking domains in cartilage type XI collagen. In

A:Reference number: A56978; MUID:95370194; PMID:7642541

A:Accession: C56978

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-23 <WGA>

C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology

C:Keywords: hydroxylysine; hydroxyproline

F:5/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental

F:6/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match
Best Local Similarity 2.4%; Score 6; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PKGPPG 16
Db 4 PKGPPG 9

RESULT 72
C41397

hypothetical protein 2 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 03-May-1994

C:Accession: C41397

R:Miller, D.A.; Lee, A.; Matsui, Y.; Chen, E.Y.; Mosses, H.L.; Derynck, R.

Mol. Endocrinol. 3, 1926-1934, 1989

A:Title: Complementary DNA cloning of the murine transforming growth factor-beta3 (TGFB

3) cDNAs.

A:Reference number: A41397; MUID:90190650; PMID:2628730

A:Accession: C41397

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-43 <MTL>

A:Cross-references: GB:M32745

Query Match
Best Local Similarity 2.4%; Score 6; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SSPFL 9

|||||
Db 19 SSPFL 24

RESULT 73

hypothetical protein yjfb - *Bacillus subtilis*
C:Species: *Bacillus subtilis*
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C:Accession: A69850
R:Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Aevelo, V.; Berter
C.; Bron, S.; Brulliet, S.; Brusch, C.V.; Caldwell, B.; Capiano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Enslin, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Gall
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holstappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y., M.; Ogawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portet
Jeger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeder, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
Leuch, M.; Tamakoshi, A.; Tanaka, T.; Terpiltra, P.; Tojnoni, A.; Tosato, V.; Uchiyama,
T.; Wintere, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Zanchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: A69850
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Residues: 1-55 <KUN>
A:Cross-references: GB:299110; GB:AL009126; NID:92633472; PIDN:CAB13069.1; PID:el183232;
A:Experimental source: strain 168
C:Genetics:
A:Gene: yjfb

Query Match

Best Local Similarity 2.4%; Score 6; DB 2; Length 55;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25 PALSYA 30
|||||

Db 4 PALSYA 9

RESULT 74

C90826
hypothetical protein ECs1579 [imported] - *Escherichia coli* (strain O157:H7, substrain R1
C:Species: *Escherichia coli*
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: C90826
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: C90826
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-63 <HAY>
A:Cross-references: PIDN:BA935002.1; PID:G13361043; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: ECs1579

Query Match

Best Local Similarity 2.4%; Score 6; DB 2; Length 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 SVALMW 33
|||||

Db 48 SVALMW 53

RESULT 75

C75627
hypothetical protein - *Deinococcus radiodurans* (strain R1)
C:Species: *Deinococcus radiodurans*
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: C75627
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Yamathavan, J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: C75627
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-71 <WHI>
A:Cross-references: GB:AE001826; NID:96460827; PIDN:AAFI2650.1; PID:96460946; TIGR:DRB0
A:Experimental source: strain R1
A:Genetics:
A:Gene: DRB0085
A:Map position: megaplasmid
A:Genome: plasmid
A:Note: plasmid MPl

Query Match

Best Local Similarity 2.4%; Score 6; DB 2; Length 71;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 162 VYLLYS 167
|||||

Db 59 VYLLYS 64

Search completed: March 26, 2003, 07:49:38
Job time : 58 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 07:37:00 ; Search time 87 Seconds

(without alignments)
592.089 Million cell updates/sec

Title: US-09-724-341-8

Perfect score: 250
Sequence: 1 MPASSPFLAPKGPNGMG.....RARKNLSPHGIFLGFVKL 250

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

rd size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeophages:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	3.2	202	16	Q8R560
2	8	3.2	223	10	Q94A26
3	8	3.2	327	16	Q8Y510
4	8	3.2	577	16	Q8R6N2
5	8	3.2	645	16	Q9RU98
6	8	3.2	773	13	P79805
7	8	2.8	76	12	Q84548
8	8	2.8	79	5	Q86487
9	8	2.8	90	6	Q9N0A0
10	8	2.8	106	8	Q9MFF2
11	8	2.8	106	12	Q9IGK6
12	8	2.8	122	11	Q9COB7
13	8	2.8	127	5	Q23503
14	8	2.8	129	10	Q94FP1
15	8	2.8	142	10	Q941A6
16	8	2.8	146	16	Q9S2C5

17	7	2.8	156	2	Q9S6G3	Q9S6G3 streptococ
18	7	2.8	156	2	Q9S6G4	Q9S6G4 streptococ
19	7	2.8	170	11	Q9DAF5	Q9DAF5 mus musculu
20	7	2.8	175	17	Q8ZWM1	Q8ZWM1 pyrobaculum
21	7	2.8	180	16	Q9RKN9	Q9RKN9 streptococ
22	7	2.8	183	10	Q9FSU6	Q9FSU6 fagus sylv
23	7	2.8	185	10	Q8S7G3	Q8S7G3 oryza sativ
24	7	2.8	192	11	Q9D5L5	Q9D5L5 mus muscul
25	7	2.8	193	11	Q9D9T6	Q9D9T6 mus muscul
26	7	2.8	200	2	Q30656	Q30656 atotobacter
27	7	2.8	217	16	Q9X5C4	Q9X5C4 streptococ
28	7	2.8	219	5	Q02210	Q02210 caenorhabd
29	7	2.8	223	16	Q9ZRX9	Q9ZRX9 thizobium m
30	7	2.8	231	10	Q94EF39	Q94EF39 arabidopsi
31	7	2.8	232	16	Q8ZXR6	Q8ZXR6 salmonella
32	7	2.8	232	16	Q8ZJM0	Q8ZJM0 yersinia pe
33	7	2.8	232	16	Q8Z2W2	Q8Z2W2 salmonella
34	7	2.8	234	16	Q8XIF6	Q8XIF6 clostridium
35	7	2.8	239	2	Q9X5C5	Q9X5C5 streptococ
36	7	2.8	244	6	Q9N0G5	Q9N0G5 philander m
37	7	2.8	255	16	Q8Z8J6	Q8Z8J6 secale cere
38	7	2.8	258	10	Q81480	Q81480 secale cere
39	7	2.8	259	17	Q974L3	Q974L3 sulfolobus
40	7	2.8	261	10	Q94H16	Q94H16 arabidopsi
41	7	2.8	265	16	Q07791	Q07791 mycobacteri
42	7	2.8	268	2	Q9X5C6	Q9X5C6 streptococ
43	7	2.8	287	5	Q20742	Q20742 caenorhabd
44	7	2.8	289	16	Q9KMW7	Q9KMW7 vibrio chol
45	7	2.8	305	2	Q8VRV3	Q8VRV3 thermodesul
46	7	2.8	314	16	Q9A3Y3	Q9A3Y3 caulobacter
47	7	2.8	326	10	Q910I8	Q910I8 arabidopsi
48	7	2.8	326	10	Q9EPK0	Q9EPK0 arabidopsi
49	7	2.8	326	10	Q9S2M6	Q9S2M6 arabidopsi
50	7	2.8	331	10	Q9XEU4	Q9XEU4 oryza sativ
51	7	2.8	335	12	Q68405	Q68405 human cyto
52	7	2.8	349	10	Q9FLV7	Q9FLV7 arabidopsi
53	7	2.8	353	17	Q9HLQ5	Q9HLQ5 thermoplas
54	7	2.8	354	17	Q97C19	Q97C19 thermoplas
55	7	2.8	359	5	Q20880	Q20880 caenorhabd
56	7	2.8	359	10	Q9LXR6	Q9LXR6 arabidopsi
57	7	2.8	360	2	Q68551	Q68551 pseudomonas
58	7	2.8	378	6	Q9N0R7	Q9N0R7 thylamys pa
59	7	2.8	379	6	Q9N0S0	Q9N0S0 gracillinu
60	7	2.8	383	10	Q91V20	Q91V20 arabidopsi
61	7	2.8	385	6	Q9N0R9	Q9N0R9 gracillinu
62	7	2.8	385	6	Q9MYN9	Q9MYN9 marosops i
63	7	2.8	386	6	Q9MYN7	Q9MYN7 marosops p
64	7	2.8	386	6	Q9MYN9	Q9MYN9 didelphis m
65	7	2.8	386	6	Q9MYN3	Q9MYN3 marosops n
66	7	2.8	386	6	Q9N0S9	Q9N0S9 caluromysio
67	7	2.8	386	6	Q9N0S8	Q9N0S8 marosops n
68	7	2.8	386	6	Q9N0S7	Q9N0S7 didelphis m
69	7	2.8	386	6	Q9N0S6	Q9N0S6 chironectes
70	7	2.8	386	6	Q9N0S5	Q9N0S5 marosops lep
71	7	2.8	386	6	Q9N0S4	Q9N0S4 didelphis a
72	7	2.8	386	6	Q9N0S3	Q9N0S3 didelphis a
73	7	2.8	386	6	Q9N0S2	Q9N0S2 lutreolina
74	7	2.8	386	6	Q9N0S8	Q9N0S8 gliconia ve
75	7	2.8	386	6	Q9N0R6	Q9N0R6 caluromys i
76	7	2.8	386	6	Q9N0R5	Q9N0R5 micoureus d
77	7	2.8	386	6	Q9N0R4	Q9N0R4 monodelphis
78	7	2.8	386	6	Q9N0R3	Q9N0R3 micoureus d
79	7	2.8	386	6	Q9N0R2	Q9N0R2 monodelphis
80	7	2.8	386	6	Q9N0R1	Q9N0R1 philander m
81	7	2.8	386	6	Q9N0R0	Q9N0R0 marosops n
82	7	2.8	386	6	Q9N0G9	Q9N0G9 marosops n
83	7	2.8	386	6	Q9N0O8	Q9N0O8 metachirus
84	7	2.8	386	6	Q9N0O7	Q9N0O7 marosops n
85	7	2.8	386	6	Q9N0O6	Q9N0O6 marosops mur
86	7	2.8	386	6	Q9N0O4	Q9N0O4 metachirus
87	7	2.8	386	6	Q9N0O3	Q9N0O3 marosops mur
88	7	2.8	386	6	Q9N0O2	Q9N0O2 leiodelphy
89	7	2.8	395	6	Q18857	Q18857 phascogale

ID	Q8RE60	PRELIMINARY	PRT	202 AA
90	01-JUN-2002 (TREMBlrel. 21, Created)			
91	01-JUN-2002 (TREMBlrel. 21, Last sequence update)			
92	01-JUN-2002 (TREMBlrel. 21, Last annotation update)			
93	Outer membrane protein.			
94	FN1265.			
95	Fusobacterium nucleatum (subsp. nucleatum).			
96	Bacteria; Fusobacteriia; Fusobacterium.			
97	NCBI_Taxid=76856;			
98	SEQUENCE FROM N.A.			
99	SEQUENCE FROM N.A.			
100	SEQUENCE FROM N.A.			

ALIGNMENTS

ID	Q8RE60	PRELIMINARY	PRT	202 AA
90	01-JUN-2002 (TREMBlrel. 21, Created)			
91	01-JUN-2002 (TREMBlrel. 21, Last sequence update)			
92	01-JUN-2002 (TREMBlrel. 21, Last annotation update)			
93	Outer membrane protein.			
94	FN1265.			
95	Fusobacterium nucleatum (subsp. nucleatum).			
96	Bacteria; Fusobacteriia; Fusobacterium.			
97	NCBI_Taxid=76856;			
98	SEQUENCE FROM N.A.			
99	SEQUENCE FROM N.A.			
100	SEQUENCE FROM N.A.			

ID	Q8RE60	PRELIMINARY	PRT	202 AA
90	01-JUN-2002 (TREMBlrel. 21, Created)			
91	01-JUN-2002 (TREMBlrel. 21, Last sequence update)			
92	01-JUN-2002 (TREMBlrel. 21, Last annotation update)			
93	Outer membrane protein.			
94	FN1265.			
95	Fusobacterium nucleatum (subsp. nucleatum).			
96	Bacteria; Fusobacteriia; Fusobacterium.			
97	NCBI_Taxid=76856;			
98	SEQUENCE FROM N.A.			
99	SEQUENCE FROM N.A.			
100	SEQUENCE FROM N.A.			

ID	Q8RE60	PRELIMINARY	PRT	202 AA
90	01-JUN-2002 (TREMBlrel. 21, Created)			
91	01-JUN-2002 (TREMBlrel. 21, Last sequence update)			
92	01-JUN-2002 (TREMBlrel. 21, Last annotation update)			
93	Outer membrane protein.			
94	FN1265.			
95	Fusobacterium nucleatum (subsp. nucleatum).			
96	Bacteria; Fusobacteriia; Fusobacterium.			
97	NCBI_Taxid=76856;			
98	SEQUENCE FROM N.A.			
99	SEQUENCE FROM N.A.			
100	SEQUENCE FROM N.A.			

ID	Q8RE60	PRELIMINARY	PRT	202 AA
90	01-JUN-2002 (TREMBlrel. 21, Created)			
91	01-JUN-2002 (TREMBlrel. 21, Last sequence update)			
92	01-JUN-2002 (TREMBlrel. 21, Last annotation update)			
93	Outer membrane protein.			
94	FN1265.			
95	Fusobacterium nucleatum (subsp. nucleatum).			
96	Bacteria; Fusobacteriia; Fusobacterium.			
97	NCBI_Taxid=76856;			
98	SEQUENCE FROM N.A.			
99	SEQUENCE FROM N.A.			
100	SEQUENCE FROM N.A.			

ID	Q8RE60	PRELIMINARY	PRT	202 AA
90	01-JUN-2002 (TREMBlrel. 21, Created)			
91	01-JUN-2002 (TREMBlrel. 21, Last sequence update)			
92	01-JUN-2002 (TREMBlrel. 21, Last annotation update)			
93	Outer membrane protein.			
94	FN1265.			
95	Fusobacterium nucleatum (subsp. nucleatum).			
96	Bacteria; Fusobacteriia; Fusobacterium.			
97	NCBI_Taxid=76856;			
98	SEQUENCE FROM N.A.			
99	SEQUENCE FROM N.A.			
100	SEQUENCE FROM N.A.			

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AC  Q8R6N2;
DT  01-JUN-2002 (TrEMBLrel. 21, Created)
DT  01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE  ABC-type multidrug/protein/lipid transport system, ATPase
DE  component.
GN  MDLB12 OR TBE2769.
OS  Thermotoga maritima.
OC  Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC  Thermotogaceae; Thermotogales; Thermotogaceae; Thermotoga.
OX  NCBI_TaxID=119072;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=MB4T / JCM11007;
RX  MEDLINE=2192816; PubMed=11997336;
RA  Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA  Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA  Tan H., Chen R., Wang J., Yu J., Yang H.;
RT  "A complete sequence of T. tengcongensis genome.";
RT  Genome Res. 12:689-700(2002).
EMBL: AB013214; AAM25873.1; -.
NC  Complete proteome.
SQ  SEQUENCE 577 AA; 66097 MW; BA6642DF1FBE7545 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 16; Length 577;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  224 ILSVIIPR 231
Db  160 ILSVIIPR 167

RESULT 5
ID  Q9RU98 PRELIMINARY; PRT; 645 AA.
AC  Q9RU98;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE  NADH dehydrogenase I, L subunit.
GN  DRI1494.
OS  Deinococcus radiodurans.
OC  Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
OC  Deinococcaceae; Deinococcus.
OX  NCBI_TaxID=1299;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=R1;
RX  MEDLINE=20036896; PubMed=10567266;
RA  White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA  Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA  Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA  Vamathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,
RA  Mekatova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA  Fraser C.M.;
RT  "Genome sequence of the radioresistant bacterium Deinococcus
RT  radiodurans R1.";
RT  Science 286:1571-1577(1999).
CC  -1- CATALYTIC ACTIVITY: NADH + URICINONE = NAD(+) + URICINOL.
CC  -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC  -1- SIMILARITY: TO NADH-URICINONE/PLASTOQUINONE (COMPLEX I), VARIOUS
CC  CHAINS.
CC  -1- SIMILARITY: TO ONE OF THE POLYPEPTIDE CHAINS OF THE NADH-URICINOL.
CC  EMBL: AB011993; AAF1057.1; -.
DR  TIGR: DR1494; -.
DR  InterPro: IPR001750; Oxidored_q1.
DR  InterPro: IPR001516; Oxidored_q1_N.
DR  Pfam: PF00361; Oxidored_q1; 1.
DR  Pfam: PF00662; Oxidored_q1_N; 1.
KW  NAD; Oxidoreductase; Transmembrane; Complete proteome.

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SQ  SEQUENCE 645 AA; 69544 MW; AB5A3493F4DDE3F6 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 16; Length 645;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  212 YSAGVFHL 219
Db  345 YSAGVFHL 352

RESULT 6
ID  P79805 PRELIMINARY; PRT; 773 AA.
AC  P79805;
DT  01-MAY-1997 (TrEMBLrel. 03, Created)
DT  01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT  01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE  Microtubule-based motor protein.
GN  FKIF2.
OS  Morone saxatilis (Striped bass).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC  Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;
OC  Moronidae; Morone.
OX  NCBI_TaxID=34816;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=RETINA;
RA  Boet-Unger L.;
RL  Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR  EMBL: U64819; AAB39558.1; -.
DR  HSSP: P17119; 3KAR.
DR  InterPro: IPR001752; Kinesin_motor.
DR  Pfam: PF00225; Kinesin; 1.
DR  PRINTS: PR00380; KINESINHEAVY.
DR  SMART: SM00129; KISC; 1.
DR  PROSITE: PS00411; KINESIN MOTOR DOMAIN1; 1.
DR  PROSITE: PS50667; KINESIN MOTOR DOMAIN2; 1.
KW  ATP-binding; Coiled coil; Microtubules; Motor protein.
SQ  SEQUENCE 773 AA; 87392 MW; B16832F0A4B0FA45 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 13; Length 773;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  57 SLREVSFR 64
Db  62 SLREVSFR 69

RESULT 7
ID  Q84548 PRELIMINARY; PRT; 76 AA.
AC  Q84548;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  A228R protein.
GN  A228R.
OS  Parametium burseria chlorella virus 1 (PBCV-1).
OC  Viruses; dsRNA viruses, no RNA stage; Phycodnaviridae; Chlorovirus.
OX  NCBI_TaxID=10506;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  MEDLINE=96187795; PubMed=8614977;
RX  Lu Z., Li Y., Que Q., Kutish G.F., Rock D.L., Van Etten J.L.;
RT  "Analysis of 94 kb of the chlorella virus PBCV-1 330-kb genome: map
RT  positions 88 to 182.";
RT  Virology 216:102-123(1996).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=20013326; PubMed=10544099;

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RA Kaiser A., Vollmert M., Tholl D., Graves M.V., Gurnon J.R., Xing W.,
 RA Lisee A.D., Nickerson K.W., Van Etten J.L.;
 RT "Chlorella virus PBCV-1 encodes a functional homospesmidine
 RT synthase.";
 RL Virology 263:254-262(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20478054; PubMed=11021991;
 RA Sun L., Gurnon J.R., Adams B.J., Graves M.V., Van Etten J.L.;
 RT "Characterization of a beta-1,3-glucanase encoded by chlorella virus
 RT PBCV-1.";
 RL Virology 276:27-36(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Van Etten J.L.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Van Etten J.L.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Van Etten J.L.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Graves M.V., Van Etten J.L.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A.
 RA Graves M.V., Van Etten J.L.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A.
 RA Gurnon J.R., Graves M.V., Van Etten J.L.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U42580; AAC96596.1; -
 SQ SEQUENCE 76 AA; 8736 MW; 36C184955635134 CRC64;
 Query Match 2.8%; Score 7; DB 12; Length 76;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 27 LSVALLML 33
 Db 69 LSVALLML 75
 RESULT 8
 ID 096487 PRELIMINARY; PRT; 79 AA.
 AC 096487;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Hydroethetical 8.0 kDa protein (Fragment).
 GN STEVOR 3D7REP-Z.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=W2;
 RX MEDLINE=99094504; PubMed=9879895;
 RA Cheng Q., Cloonan N., Fischer K., Thompson J., Wayne G., Lanzer M.,
 RA Saul A.;
 RT "Sevior and rif are Plasmodium falciparum multicopy gene families
 RT which potentially encode variant antigens.";
 RL Mol. Biochem. Parasitol. 97:161-176(1998).
 DR EMBL; AF065197; AAD03647.1; -
 DR InterPro; IPR002858; Rifin_STEVOR.
 DR Pfam; PF02009; Rifin_STEVOR; 1.
 KW Hypothetical protein.

FT NON_TER 1 1
 FT NON_TER 79 79
 SQ SEQUENCE 79 AA; 7981 MW; D17FF8DB0938F414 CRC64;
 Query Match 2.8%; Score 7; DB 5; Length 79;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 37 AALGAVA 43
 Db 17 AALGAVA 23
 RESULT 9
 ID 09NOA0 PRELIMINARY; PRT; 90 AA.
 AC 09NOA0;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE Unnamed protein product.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Osada N., Hida M., Kuenda J., Tanuma R., Iseki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RT "Isolation of full-length cDNA clones from macaque brain cDNA
 RT libraries.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB046030; BAB01612.1; -
 SQ SEQUENCE 90 AA; 9689 MW; 4F33636A3DF27274 CRC64;
 Query Match 2.8%; Score 7; DB 6; Length 90;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 ALGAVAC 44
 Db 67 ALGAVAC 73
 RESULT 10
 ID 09MFP2 PRELIMINARY; PRT; 106 AA.
 AC 09MFP2;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE Orf106a protein.
 GN ORF106A.
 OS Beta vulgaris (Sugar beet).
 OC Beta vulgaris.
 OC Mitochondrion.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.
 OX NCBI_TaxID=3555;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TK81-O;
 RX MEDLINE=20330382; PubMed=10871408;
 RA Kubo T., Nishizawa S., Sugawara A., Itchoda N., Esitachi A., Mikami T.;
 RT "The complete nucleotide sequence of the mitochondrial genome of sugar
 RT beet (Beta vulgaris L.) reveals a novel gene for tRNACys(GCA).";
 RL Nucleic Acids Res. 28:2571-2576(2000).
 DR EMBL; AP000396; BAA92290.1; -
 KW Mitochondrion.
 SQ SEQUENCE 106 AA; 11906 MW; 31B09126047F8602 CRC64;
 Query Match 2.8%; Score 7; DB 8; Length 106;

Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ASFFLL 9
|||||
Db 67 ASFFLL 73

RESULT 11

09IGK6 PRELIMINARY; PRT; 106 AA.
AC 09IGK6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Type II envelope protein US9.
OS Pseudorabies virus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
NCBI_TaxID=10345;
[1]

SEQUENCE FROM N.A.

RC STRAIN=BA;
RT "Cloning and Expression of I1K gene of Pseudorabies Virus Strain Ba."
RL Submitted (A9R-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF251220; AAF86961.1; -
KM Envelope protein.
SQ SEQUENCE 106 AA; 11337 MW; .69FD0FEBB3529066 CRC64;

Query Match 2.8%; Score 7; DB 12; Length 106;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LLAPKGP 14
|||||
Db 30 LLAPKGP 36

RESULT 12

09COB7 PRELIMINARY; PRT; 122 AA.
AC 09COB7;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE 4930404J24R1K protein (2310004B22R1K protein) (RIKEN CDNA 2310004B22 gene).
4930404J24R1K OR 2310004B22R1K.

Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=TESTIS, AND TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamahata I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiraldi L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Kono H., Baldarelli R., Barsh G.,
RA Blake J., Botfield D., Bjung N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guenichon S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Wells C., Wittaker C., Wilming L.,

RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [2]

SEQUENCE FROM N.A.

RA Strausberg R.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK015083; BAB29706.1; -
DR EMBL; AK009135; BAB26096.1; -
DR EMBL; BC011339; AAH11339.1; -
DR MGD; MGI:1921169; 4930404J24R1K.
DR MGD; MGI:1923685; 2310004B22R1K.
SQ SEQUENCE 122 AA; 14223 MW; A2E020FDEA355E9 CRC64;

Query Match 2.8%; Score 7; DB 11; Length 122;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 143 RRGRLQ 149
|||||
Db 95 RRGRLQ 101

RESULT 13

023503 PRELIMINARY; PRT; 127 AA.
AC 023503;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hypothetical 14.6 kDa protein.
GN ZK470.3.
OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodetrinae; Caenorhabditis.
NCBI_TaxID=6239;

RA None;
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;

RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]

SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;
RA Mink M.,
RT "The sequence of C. elegans cosmid ZK470."
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.,
RT "Direct Submission."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U93651; AAA80393.1; -
KW Hypothetical protein.
SQ SEQUENCE 127 AA; 14574 MW; 0497D03C31D4E403 CRC64;

Query Match 2.8%; Score 7; DB 5; Length 127;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 LQSLRRE 61
|||||
Db 109 LQSLRRE 115

RESULT 14

094FPI PRELIMINARY; PRT; 129 AA.

AC Q94FP1;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Succinate dehydrogenase subunit 3.
 GN SDH3.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriocarpaceae; Oryzaceae; Oryza.
 NC NCB1_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21347578; PubMed=11454775;
 RA Adams K.L., Rosenbluth M., Qiu Y.L., Palmer J.D.;
 RT "Multiple losses and transfers to the nucleus of two mitochondrial
 succinate dehydrogenase genes during angiosperm evolution";
 RL Genetics 158:1289-1300(2001).
 DR EMBL; AF362742; AAK73695.1; -.
 InterPro; IPR000701; Sdh_cyt.1.
 Pfam; PF01127; Sdh_cyt.1.
 SEQUENCE 129 AA; 13863 MW; 761285B86EA4B204 CRC64;

Query Match 2.8%; Score 7; DB 10; Length 129;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 36 GAALGAV 42
 Db 107 GAALGAV 113

RESULT 15

Q941A6 PRELIMINARY; PRT; 142 AA.

ID Q941A6;
 AC Q941A6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Actinobaculum (mouse ear cress).
 OS Arabidopsis thaliana (mouse ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 NC NCB1_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
 Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,
 Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
 Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
 Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
 Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
 Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RA "Arabidopsis cDNA clones";
 RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
 Bowser L., Carninci P., Chang B., Dale J.M., Goldsmith A.D.,
 Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
 Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
 Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
 Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 Ecker J.R.;
 RT "Arabidopsis ORF clones";
 RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY052314; AAK96507.1; -.
 DR EMBL; AY051894; AAL31221.1; -.
 SO SEQUENCE 142 AA; 15813 MW; 011B57628991D235 CRC64;

Query Match 2.8%; Score 7; DB 10; Length 142;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 36 GAALGAV 42
 Db 74 GAALGAV 80

RESULT 16

Q9S2C5 PRELIMINARY; PRT; 146 AA.

ID Q9S2C5;
 AC Q9S2C5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical protein SC00288.
 GN SC00288 OR SCF85.16.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 NC NCB1_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 Cronin A., Fraser A., Goble A., Hidalgo J., Hornby T., Howarth S.,
 Huang C.H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S., Taylor K.,
 Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 Warren T., Wietzorrek A., Woodward J., Barrall B.G., Parkhill J.,
 Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL; AL110470; CAB54173.1; -.
 KW Hypothetical protein.
 SEQUENCE 146 AA; 14974 MW; 4350B8BEF04315B6 CRC64;

Query Match 2.8%; Score 7; DB 16; Length 146;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 37 AALGAVA 43
 Db 48 AALGAVA 54

RESULT 17

Q9S6G3 PRELIMINARY; PRT; 156 AA.

ID Q9S6G3;
 AC Q9S6G3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE GRAB (Fragment).
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 NC NCB1_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=API;
 RX MEDLINE=99269061; PubMed=10336419;
 RA Raemussen M., Muller H.P., Bjorck L.;
 RT "Protein GRAB of streptococcus pyogenes regulates proteolysis at the
 bacterial surface by binding alpha2-macroglobulin.";
 RL J. Biol. Chem. 274:15336-15344(1999).
 DR EMBL; AF124400; AAD26339.1; -.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.

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FT  NON_TER 1 1
FT  NON_TER 156 156
SQ  SEQUENCE 156 AA; 16587 MW; 19FAA98D0599D866 CRC64;

Query Match
Best Local Similarity 2.8%; Score 7; DB 2; Length 156;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 SSDALEA 93
    |||||
    58 SSDALEA 64

RESULT 18
Q9S6G4 PRELIMINARY; PRT; 156 AA.
ID Q9S6G4;
AC Q9S6G4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RT GRAB (Fragment).
RL J. Biol. Chem. 274:15336-15344(1999).
DR InterPro: IPR001899; Gram pos anchor.
DE PROSITE, PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
FT NON_TER 1 1
FT NON_TER 156 156
SQ SEQUENCE 156 AA; 16575 MW; 0C20967E2F80D866 CRC64;

Query Match
Best Local Similarity 2.8%; Score 7; DB 2; Length 156;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 SSDALEA 93
    |||||
    58 SSDALEA 64

SULT 19
Q9DAF5 PRELIMINARY; PRT; 170 AA.
ID Q9DAF5;
AC Q9DAF5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 1700011N12RIK protein.
GN 1700011N12RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atsawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

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RA Schirml L.M., Straubi F., Suzuki R., Tomita M., Wagner L., Maehio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carinci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Maehima J., Mazzarelli J., Mombaerts P.,
RA Nodone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohenki S.,
RA Hasehizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK005880; BAB24295.1; -.
DR MGD; MGI:1916552; 1700011N12RIK.
DR InterPro: IPR002965; P rich extensn.
DR PRINTS; PRO1217; PRICHEXTENS.
SQ SEQUENCE 170 AA; 18852 MW; 4D4317B1A8A94581 CRC64;

Query Match
Best Local Similarity 2.8%; Score 7; DB 11; Length 170;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PASSPFL 8
    |||||
    80 PASSPFL 86

RESULT 20
Q8ZWM1 PRELIMINARY; PRT; 175 AA.
ID Q8ZWM1;
AC Q8ZWM1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE P. aerophilum family 550 protein.
GN PAE1719.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX PubMed=11792869;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AE009836; AAL63680.1; -.
KW Complete proteome.
SQ SEQUENCE 175 AA; 19680 MW; 8EDA0DD7474FBBB5 CRC64;

Query Match
Best Local Similarity 2.8%; Score 7; DB 17; Length 175;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 PALSVL 31
    |||||
    147 PALSVL 153

RESULT 21
Q9RKN9 PRELIMINARY; PRT; 180 AA.
ID Q9RKN9;
AC Q9RKN9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative membrane protein.
GN SCO2289 OR SCCT5A.35.
OS Streptomyces coelicolor.

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OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxId=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA Bertley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleiser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleiser T., Latke L., Murphy L., Oliver K., O'Neil S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; ALJ33220; CAB61735.1; -.
SQ SEQUENCE 180 AA; 17710 MW; 57C052F39D4E0BDF CRC64;

Query Match 2.8%; Score 7; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 188 GROETLF 194
|||||
Db 173 GROETLF 179

RESULT 22
O9FSU6 PRELIMINARY; PRT; 183 AA.
ID O9FSU6;
AC O9FSU6;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Protein phosphatase 2C (PP2C) (Fragment).
GN PP2CFL.
OS Fagus sylvatica (Beechnut).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fagales; Fagaceae; Fagus.
OX NCBI_TaxId=28930;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SEED;
RA Lorenzo O.;
RA Thesis (2000), Fisiologia Vegetal, Facultad de Biologia,
RA Universidad de Salamanca.
RA EMBL; AJ298987; CAC09575.1; -.
DR HSSP; P35813; IAGO.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2Cc; 1.
FT NON_TER 1
FT TER 183
SQ SEQUENCE 183 AA; 20365 MW; C9BA9F770EAFFB0 CRC64;

Query Match 2.8%; Score 7; DB 10; Length 183;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 155 VRIODAG 161
|||||
Db 120 VRIODAG 126

RESULT 23
O8S7G3 PRELIMINARY; PRT; 185 AA.
ID O8S7G3;
AC O8S7G3;
DT 01-JUN-2002 (TREMBlrel. 21, Created)

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DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypoetical 19.5 kDa protein.
GN OSUNB0048D20.11.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxId=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Buehl C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
RA Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
RA Tselirin T., Riggs F., Hsiao J., Ziemann V., Blunt S., Pai G.,
RA Vanaken S.E., Uteback T.R., Feldblyum T.V., Kalb E., Quackenbush J.,
RA Salzberg S.L., White O., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSUNB0048D20 genomic sequence.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC084766; AL82525.1; -.
KM Hypoetical protein.
SQ SEQUENCE 185 AA; 19508 MW; 7FF8D336DF819FC CRC64;

Query Match 2.8%; Score 7; DB 10; Length 185;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 ASSPFL 9
|||||
Db 6 ASSPFL 12

RESULT 24
O9D5L5 PRELIMINARY; PRT; 192 AA.
ID O9D5L5;
AC O9D5L5;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 17, Last annotation update)
DE 4930424D10R1k protein.
GN 4930424D10R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Irawa M., Nishi K., Kiyosawa H., Kondo S., Yamano I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Baren G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bona M.F.,
RA Brownstein M.J., But C., Fletcher C., Fujita M., Gariboldi M.,
RA Guenichon S., Hill D., Hofmann M., Hune D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombauts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilting L.,
RA Wyshaw-Boris A., Yoshida K., Haegawa Y., Kawaji H., Kontseki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK015193; BA829741.1; -.
DR MGI; MGI:1921026; 4930424D10R1k.
DR InterPro; IPR002965; P-rich_extensn.
DR PRINTS; PRO1217; PRICHEXTNSN.

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SO SEQUENCE 192 AA; 20876 MW; 4CCA5438516F24E9 CRC64;
Query Match 2.8%; Score 7; DB 11; Length 192;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PASSPFL 8
DB 80 PASSPFL 86

RESULT 25
Q9D9T6 PRELIMINARY; PRT; 193 AA.
AC Q9D9T6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE 1700029H01Rik protein.
1700029H01Rik.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
Saito T., Okazaki Y., Gajdosi T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
R. Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
Kuehl P., Lewis S., Matsuo Y., Nakai I., Pesole G., Quackenbush J.,
Schrödl L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Watanabe T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barin G.,
Blake J., Botfield D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
Guentlich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nodone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
Wynshaw-Borle A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL: AK006491; BAB24616.1;
MGD: MGI:1917310; 1700029H01Rik.
InterPro: IPR002965; P rich exten.
DR PRINTS: PR01217; PRICHXTENSN.
SO SEQUENCE 193 AA; 20948 MW; 91333BECF952AE229 CRC64;

Query Match 2.8%; Score 7; DB 11; Length 193;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PASSPFL 8
DB 80 PASSPFL 86

RESULT 26
Q30656 PRELIMINARY; PRT; 200 AA.
AC Q30656;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-JAN-1998 (TREMBlrel. 05, Last annotation update)
DE Hypothetical 22.5 kDa protein.
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;

OC Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TRANS;
RA Dean D.R.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF014048; AAB6329.1;
KM Hypothetical protein.
SO SEQUENCE 200 AA; 22517 MW; 608FEDC5BB8FA0 CRC64;

Query Match 2.8%; Score 7; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 SSPFLA 10
DB 190 SSPFLA 196

RESULT 27
Q9X5C4 PRELIMINARY; PRT; 217 AA.
AC Q9X5C4;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE GRAB precursor (Protein GRAB) (Protein G-related alpha 2M-binding
protein).
GN GRAB OR SPY1357.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
CX Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC700294;
RA Rasmussen M., Muller H.P., Bjorck L.;
RT "Protein GRAB of Streptococcus pyogenes regulates proteolysis at the
bacterial surface by binding alpha2-macroglobulin.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Perrecci J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
Primeaux C., Szate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
Ran Y., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
DR EMBL: AF24399; AAD26338.1;
DR EMBL: AB006573; AKK34185.1;
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR PRINTS: PR00015; GPOSANCHOR.
DR TIGRPFAM: TIGR01167; LPXG anchor; 1.
DR PROSITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
KW Signal; Transmembrane; Complete proteome.
FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 217 GRAB.
SO SEQUENCE 217 AA; 22836 MW; 79AAB8CAF5F3FA06 CRC64;

Query Match 2.8%; Score 7; DB 16; Length 217;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 87 SSDALFA 93
DB 91 SSDALFA 97

RESULT 28

002210
ID 002210 PRELIMINARY; PRT; 219 AA.
AC 002210;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
GN C01A2.6 protein.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN 11
RP SEQUENCE FROM N.A.
RA Kershaw J.K.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN 12
RP SEQUENCE FROM N.A.
RA MEDLINE=99069613; PubMed=9851916;
RX none;
RL "Genome sequence of the nematode C.elegans: A platform for
investigating biology";
DR EMBL; Z81029; CAB02701.1; -;
SQ SEQUENCE 219 AA; 25378 MW; B8C585E206275853 CRC64;
Query Match 2.8%; Score 7; DB 5; Length 219;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 91 LEAWENG 97
DB 85 LEAWENG 91
RESULT 29
Q92R91
ID Q92R91 PRELIMINARY; PRT; 223 AA.
AC Q92R91;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE Probable transcription regulator protein.
GN FEUP OR R01014 OR SMC000458.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
RX NCBI_TaxID=382;
[1]
SEQUENCE FROM N.A.
RC STRAIN=1021;
RA MEDLINE=21396507; PubMed=11481430;
RA Bozard D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Boisard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
Goffie T., Goffeau A., Kahn D., Kise E., Lelaue V., Masny D.,
Pohl T., Portetlelle D., Puhler A., Purnelle B., Rampeger U.,
Renard C., Trebault P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
Sinorhizobium meliloti strain 1021";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591785; CAC45586.1; -;
DR InterPro; IPR001789; Response_reg.
DR InterPro; IPR003662; sub transporter.
DR InterPro; IPR001867; Trans_reg_C.
DR Pfam; PF00072; response_reg_1.
DR Pfam; PF00486; trans_reg_C_1.
DR ProDom; PD000039; Response_reg_1.
DR ProDom; PD000039; Trans_reg_C_1.
DR PROSITE; PS00217; SUGAR_TRANSPORT_2; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 223 AA; 24786 MW; 8B4C7C1B34A74CF8 CRC64;
Query Match 2.8%; Score 7; DB 16; Length 223;

Best Local Similarity 100.0%; Pred. No. 80;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 178 MGQVSR 184
DB 165 MGQVSR 171
RESULT 30
Q94F39
ID Q94F39 PRELIMINARY; PRT; 231 AA.
AC Q94F39;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE ATG92975/MME13.2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN 11
RP SEQUENCE FROM N.A.
RA Shum P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
RA Tracy S.E., Banb J., Bowser L., Carninci P., Chung M.K.,
RA Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Natsusaka M., Nguyen M., Palm C.J., Pham P.K., Quach H.L.,
RA Sakano H., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C.,
RA Toriumi M., Yamada K., Yu G., Shinzaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF385741; AAK60331.1; -;
SQ SEQUENCE 231 AA; 25243 MW; 7CE5267AC501012D CRC64;
Query Match 2.8%; Score 7; DB 10; Length 231;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 54 ELOSIR 60
DB 74 ELOSIR 80
RESULT 31
Q8ZKR6
ID Q8ZKR6 PRELIMINARY; PRT; 232 AA.
AC Q8ZKR6;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Response regulator in two-component regulatory system with CpxA,
DE regulates expression of protein folding and degradation factors (OmpR
family).
GN CPXR OR STM4059.
OS Bacteria; Proteobacteria.
OC Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=L72 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Portolillo S., Ali J., Dante M., Du P., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2";
RL Nature 413:852-856(2001).
DR EMBL; AE008889; AAL22899.1; -;

DR InterPro; IPR001789; Response_reg.
 DR InterPro; IPR001867; Trans_reg_C.
 DR Pfam; PF00072; Response_reg; 1.
 DR Pfam; PF00486; Trans_reg_C; 1.
 DR ProDom; PD000039; Response_reg; 1.
 DR ProDom; PD000329; Trans_reg_C; 1.
 DR SMART; SM00448; REC; 1.
 DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
 DR Complete proteome.
 KW SEQUENCE 232 AA; 26274 MW; 1873AF5CC59B44A CRC64;

Query Match 2.8%; Score 7; DB 16; Length 232;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 179 GOVSRE 185
 |||||
 Db 173 GOVSRE 179

SUPT 32

082JMO PRELIMINARY; PRT; 232 AA.

DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Two component system response regulatory protein.
 GN CPYR OR YPO0074.
 OS Yersinia pestis.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Yersinia.
 OX NCBI_TaxID=632;
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CO-92 / BIOVAR ORIENTALIS;
 RX MEDLINE=21470413; PubMed=11586360;
 RA Parkhill J., Wren B.W., Thomson N.R., Titchell R.W., Holden M.T.G.,
 RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Felwell T., Hamlin N., Holtroyd S., Jagers K., Kariyeh A.V.,
 RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
 RT "Genome sequence of Yersinia pestis, the causative agent of plague."
 RL Nature 413:523-527(2001).

DR EMBL; AJ14141; CAC8940.1; -
 DR InterPro; IPR001789; Response_reg.
 DR InterPro; IPR001867; Trans_reg_C.
 DR Pfam; PF00072; Response_reg; 1.
 DR Pfam; PF00486; Trans_reg_C; 1.
 DR ProDom; PD000039; Response_reg; 1.
 DR ProDom; PD000329; Trans_reg_C; 1.
 DR SMART; SM00448; REC; 1.
 DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
 DR Complete proteome.
 KW SEQUENCE 232 AA; 26495 MW; 14AB928B0806884A CRC64;

Query Match 2.8%; Score 7; DB 16; Length 232;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 179 GOVSRE 185
 |||||
 Db 173 GOVSRE 179

RESULT 33

0822W2 PRELIMINARY; PRT; 232 AA.

DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Two-component response regulatory protein.
 GN STY3812.
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCBI_TaxID=601;
 RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21534947; PubMed=11677608;
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Felwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagers K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrell B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typhi CT18."
 RL Nature 413:848-852(2001).

DR EMBL; AL627279; CAD09565.1; -
 DR InterPro; IPR001789; Response_reg.
 DR InterPro; IPR001867; Trans_reg_C.
 DR Pfam; PF00072; Response_reg; 1.
 DR Pfam; PF00486; Trans_reg_C; 1.
 DR ProDom; PD000039; Response_reg; 1.
 DR ProDom; PD000329; Trans_reg_C; 1.
 DR SMART; SM00448; REC; 1.
 DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
 DR Complete proteome.
 KW SEQUENCE 232 AA; 26301 MW; 975DF7F5D0887041 CRC64;

Query Match 2.8%; Score 7; DB 16; Length 232;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 179 GOVSRE 185
 |||||
 Db 173 GOVSRE 179

RESULT 34

08XIF6 PRELIMINARY; PRT; 234 AA.

DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Probable glycoprotein endopeptidase.
 GN CPE2165.

OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Clostridiaceae; Clostridium.
 OX NCBI_TaxID=1502;
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=13 / TYPE A;
 RX PubMed=1179842;
 RA Shimizu T., Ohnishi K., Hiyakawa H., Ohshima K., Yamashita A.,
 RA Shiba T., Ogasawara N., Hattori M., Kubara S., Hayashi H.;
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic
 RT flesh-eater."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).

DR EMBL; AP003193; BAB81871.1; -
 DR InterPro; IPR000905; Peptidase_M22.
 DR ProDom; PD002367; Peptidase_M22; 1.
 DR Complete proteome.
 KW SEQUENCE 234 AA; 25491 MW; CA01BF26760D2621 CRC64;

Query Match 2.8%; Score 7; DB 16; Length 234;
 Best Local Similarity 100.0%; Pred. No. 84;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 112 KKHSHVL 118
|||||
DB 32 KKHSHVL 38

RESULT 35

09XSC5 PRELIMINARY; PRT: 239 AA.

AC 09XSC5: 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
[1]

SEQUENCE FROM N.A.
STRAIN-KTL9;

RA MEDLINE=99269061; Pubmed=10336419;
RA Raemussen M., Muller H.P., Bjorck L.;
RT "Protein GRAB of streptococcus pyogenes regulates proteolysis at the
bacterial surface by binding alpha2-macroglobulin."
RL J. Biol. Chem. 274:15336-15344 (1999).
DR EMBL; AF124402; AAD26341.1; -
DR InterPro; IPR001897; Gram_pos_anchor;
DR PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
FT NON TER 1
SQ SEQUENCE 239 AA; 24846 MW; 61AC4F6F63AF0F5 CRC64;

Query Match 2.8%; Score 7; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 85;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 87 SSDALEA 93
|||||
DB 58 SSDALEA 64

RESULT 36

09NOO5 PRELIMINARY; PRT: 244 AA.

AC 09NOO5: 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Interphotoreceptor retinoid binding protein (Fragment).
GN IRBP.
OS Philander mcIlhenryi.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Philander.
OX NCBI_TaxID=42729;
[1]

SEQUENCE FROM N.A.

RA Jansa S.A., Voss R.S.;
RT "Phylogenetic studies on didelphid marsupials I. Introduction and
preliminary results from nuclear IRBP gene sequences."
RL J. Mammal. Evol. 7:43-77 (2000).
DR EMBL; AF257706; AAF7203.1; -
DR InterPro; IPR003581; TSPC.
DR Pfam; PF02692; IRBP; 1.
DR SMART; SM00245; TSPC; 1.
KW Receptor.
FT NON TER 1
SQ SEQUENCE 244 AA; 26802 MW; 0948A8E3979E0E85 CRC64;

Query Match 2.8%; Score 7; DB 6; Length 244;
Best Local Similarity 100.0%; Pred. No. 87;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 219 LHOGDIL 225
|||||
DB 141 LHOGDIL 147

RESULT 37

08ZBJ6 PRELIMINARY; PRT: 255 AA.

AC 08ZBJ6: 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Molybdopterin-containing oxidoreductase membrane anchor subunit.
GN SRY0661.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;
[1]

SEQUENCE FROM N.A.

RC STRAIN=CT18;
RA MEDLINE=21534947; Pubmed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Baaham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltham T., Hamlin N., Hague A., Hien T.T., Holtroyd S., Jagels K.,
RA Krogan A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18."
RL Nature 413:848-852 (2001).
DR EMBL; AL627267; CAD05090.1; -
KW Complete proteome.
SQ SEQUENCE 255 AA; 27606 MW; CCD602E40097FC5A CRC64;

Query Match 2.8%; Score 7; DB 16; Length 255;
Best Local Similarity 100.0%; Pred. No. 91;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 203 HPDRAYN 209
|||||
DB 61 HPDRAYN 67

RESULT 38

081480 PRELIMINARY; PRT: 258 AA.

AC 081480: 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Thioredoxin peroxidase.
GN TPX1.
OS Secale cereale (Rye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Secale.
OX NCBI_TaxID=4550;
[1]

SEQUENCE FROM N.A.

RA MEDLINE=99056866; Pubmed=9867602;
RA Berberich T., Uebeler M., Feterabend J.;
RT "Cloning of a cDNA Encoding a Thioredoxin Peroxidase Homolog from
Winter Rye (Accession No. AF076920) (PGR98-167)."
RL Plant Physiol. 118:711-711 (1998).
DR EMBL; AF076920; AAC78473.1; -
DR HSSP; P30041; IPRX.
DR InterPro; IPR000866; AhpC-TSA.
DR Pfam; PF00578; AhpC-TSA; 1.

KM Peroxidase. 258 AA; 28133 MW; 9C3BD415FE8DA9A8 CRC64;
SQ SEQUENCE

Query Match 2.8%; Score 7; DB 10; Length 258;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 140 PALRRGR 146
|||
Db 32 PALRRGR 38

RESULT 39

O974L3 PRELIMINARY; PRT; 259 AA.

AC O974L3;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Putative pyrroline-5-carboxylate reductase.
ST0646.

OC Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.

OX NCBI_TaxID=111955;

RP SEQUENCE FROM N.A.

RC STRAIN=JCM 10545 / 7;

RX PubMed=11572479;

RA Kwararbyasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshitawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagishi M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;

RT "Complete genome sequence of an aerobic thermophilic
RT Crenarchaeon, Sulfolobus tokodaii strain 7.";

RL DNA Res. 8:123-140(2001).

DR EMBL; AP000983; BAB5645.1; -.

DR InterPro; IPR00304; PSCR.

DR Pfam; PF01089; PSCR. 1.

DR PROSITE; PS00521; PSCR; UNKNOWN_1.

KM Hypothetical protein; Complete proteome.

SQ SEQUENCE 259 AA; 28476 MW; 3A9614D4A6BFP936 CRC64;

Query Match 2.8%; Score 7; DB 17; Length 259;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

38 ALGAVAC 44
|||
Db 172 ALGAVAC 178

RESULT 40

O9LH16 PRELIMINARY; PRT; 261 AA.

AC O9LH16;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE Similarity to unknown protein.
DE Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RP SEQUENCE FROM N.A.

RC STRAIN=COLUMBIA;

RA Nakamura Y.;

RT "Structural Analysis of Arabidopsis thaliana Chromosome 3. III.";
Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AP002457; BAB01982.1; -.
SQ SEQUENCE 261 AA; 28447 MW; 0F7715A05845367D CRC64;

Query Match 2.8%; Score 7; DB 10; Length 261;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 54 ELQSLRR 60
|||
Db 74 ELQSLRR 80

RESULT 41

O07791 PRELIMINARY; PRT; 265 AA.

AC O07791;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Hypothetical protein RV0587.
GN RV0587 OR MTCY19H5.35C OR MT0616.

OS Mycobacterium tuberculosis.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

OX NCBI_TaxID=1773;

RP SEQUENCE FROM N.A.

RC STRAIN=H37RV;

RX MEDLINE=98295987; PubMed=9634230;

RA Cole S.T., Broesch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigler K., Gass S., Berry C.E. III, Tekala F.,
RA Badcock K., Baaham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby J., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;

RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";

RL Nature 393:537-544(1998).

DR EMBL; Z97182; CAB09951.1; -.

DR EMBL; AE006958; AAK44840.1; -.

DR TIGR; MT0616; -.

DR TubercuList; RV0587; -.

DR InterPro; IPR003453; DUF140.

DR Pfam; PF02405; DUF140; 1.

KM Hypothetical protein; Complete proteome.

SQ SEQUENCE 265 AA; 27327 MW; 1632EB79C500CD44 CRC64;

Query Match 2.8%; Score 7; DB 16; Length 265;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

36 GAALGAV 42
|||
Db 92 GAALGAV 98

RESULT 42

O9X5C6 PRELIMINARY; PRT; 268 AA.

AC O9X5C6;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Hypothetical protein RV0587.
GN RV0587 OR MTCY19H5.35C OR MT0616.

OS Mycobacterium tuberculosis.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

OX NCBI_TaxID=1773;

RP SEQUENCE FROM N.A.

RC STRAIN=H37RV;

RA Cole S.T., Broesch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigler K., Gass S., Berry C.E. III, Tekala F.,
RA Badcock K., Baaham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby J., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;

RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";

RL Nature 393:537-544(1998).

DR EMBL; Z97182; CAB09951.1; -.

DR EMBL; AE006958; AAK44840.1; -.

DR TIGR; MT0616; -.

DR TubercuList; RV0587; -.

DR InterPro; IPR003453; DUF140.

DR Pfam; PF02405; DUF140; 1.

KM Hypothetical protein; Complete proteome.

SQ SEQUENCE 265 AA; 27327 MW; 1632EB79C500CD44 CRC64;

```

DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GRAB (Fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AP49;
RX MEDLINE=99269061; PubMed=10336419;
RA Raemussen M., Muller H.P., Bjorck L.;
RT "Protein GRAB of streptococcus pyogenes regulates proteolysis at the
bacterial surface by binding alpha2-macroglobulin.";
RL J. Biol. Chem. 274:15336-15344(1999).
DR EMBL; AF124403; AAD26342.1.-.
DR InterPro; IPR001899; Gram_pos_anchor.
DR PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
NON_TER 1
SEQUENCE 268 AA; 27744 MW; 1C5923926C0C7E7 CRC64;

Query Match 2.8%; Score 7; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 SSDALEA 93
DB 58 SSDALEA 64

RESULT 43
Q20742 PRELIMINARY; PRT; 287 AA.
AC Q20742;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE F54B11.7 protein.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Swaburne J.;
RT Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
RT Science 282:2012-2018(1998).
RL EMBL; Z70208; CA94139.1.-.
SO SEQUENCE 287 AA; 31550 MW; 1B6EC2894784A3C4 CRC64;

Query Match 2.8%; Score 7; DB 5; Length 287;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 DSDVTE 135
DB 52 DSDVTE 58

RESULT 44
Q9KNW7 PRELIMINARY; PRT; 289 AA.
AC Q9KNW7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)

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DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Phosphoribulokinase.
OS VCB613.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Holt D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Ureback T., Fleischmann R.D., Nieman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
cholerae.";
RL Nature 406:477-483(2000).
DR EMBL; AE004328; AAF95754.1.-.
DR HSSP; P12033; 1A7J.
DR TIGR; VC2613; -.
DR InterPro; IPR001324; PRK.
DR Pfam; PF00485; PRK_1.
DR PRINTS; PR00478; PRIBLKNASE.
KM Kinase; Complete proteome.
SO SEQUENCE 289 AA; 32785 MW; 219167F5C61E181 CRC64;

Query Match 2.8%; Score 7; DB 16; Length 289;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 PWOSLPE 85
DB 116 PWOSLPE 122

RESULT 45
Q8VR3 PRELIMINARY; PRT; 305 AA.
AC Q8VR3;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Adenosine-5'-phosphosulfate reductase alpha subunit (Fragment).
GN APSA.
OS Thermodesulfobrio islandicus.
OC Bacteria; Nitrospirae; Nitrospirales; Nitrospiraceae;
OC Thermodesulfobrio.
OX NCBI_TaxID=53423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 12570;
RX MEDLINE=21617390; PubMed=11741869;
RA Friedrich M.W.;
RT "Phylogenetic Analysis Reveals Multiple Lateral Transfers of
Adenosine-5'-Phosphosulfate Reductase Genes among Sulfate-Reducing
Microorganisms.";
RL J. Bacteriol. 184:278-289(2002).
DR EMBL; AF148113; AAL57380.1.-.
FT NON_TER 1
FT NON_TER 1
SEQUENCE 305 AA; 34078 MW; DEB25675D4E24816 CRC64;

Query Match 2.8%; Score 7; DB 2; Length 305;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 SREGGR 189
DB 171 SREGGR 177

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RESULT 46
 ID 09A3Y3 PRELIMINARY; PRT: 314 AA.
 AC 09A3Y3; 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Peptidyl-prolyl cis-trans isomerase family protein.
 GN CC3067.
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
 OC Caulobacter.
 NCBI_Taxid=155892;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 19089 / CB15;
 RX MEDLINE=21173698; PubMed=11259647;
 RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 Pockock I., Nelson W.C., Newton A., Stephens C., Phadok N.D., Ely B.,
 DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Berry K.,
 Kolony J.F., Sait J., Craven M.B., Khouri H., Shetty J., White O.,
 Raebler S.L., Venter J.C., Shapiro L., Fraser C.M.,
 "Complete genome sequence of Caulobacter crescentus."
 RA Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 RL EMBL: AE005970; AK25029.1;
 DR TIGR: CC3067.
 DR InterPro: IPR00297; Rotamase.
 DR Pfam: PF00639; Rotamase.1.
 DR PROSITE: PS01096; PIC_PPIASE_1; UNKNOWN_1.
 DR PROSITE: PS01098; PIC_PPIASE_2; 1.
 KM Isomerase; Complete proteome.
 SQ SEQUENCE 314 AA; 33652 MW; B7A928985D323AB CRC64;

Query Match 2.8%; Score 7; DB 16; Length 314;
 Best Local Similarity 100.0%; Pred. No. 1.le+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 LGAVACA 45
 |||||
 Db 4 LGAVACA 10

RESULT 47
 ID 039108 PRELIMINARY; PRT: 326 AA.
 AC 039108; 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Geranylgeranyl pyrophosphate synthase-related protein precursor.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Scolnik P.A., Bartley G.E.;
 "Nucleotide sequence of a putative geranylgeranyl pyrophosphate
 synthase (GenBank L40577) from Arabidopsis (PCR95-018).";
 RL Plant Physiol. 108:1343-1343(1995).
 DR EMBL: L40577; AAA81879.1;
 DR InterPro: IPR000092; Polyprenyl_synth.
 DR Pfam: PF00348; polyprenyl_synth.1.
 DR PROSITE: PS00723; POLYPRENYL_SYNTHET_1; 1.
 KM Transic peptide.
 FT TRANSIT 1 47 POTENTIAL.
 FT CHAIN 48 326 GERANYLGERANYL PYROPHOSPHATE SYNTHASE-

FT SQ SEQUENCE 326 AA; 35240 MW; FF9224BCC2D7B570 CRC64;
 RELATED PROTEIN.
 Query Match 2.8%; Score 7; DB 10; Length 326;
 Best Local Similarity 100.0%; Pred. No. 1.le+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 ELQSLRR 60
 |||||
 Db 242 ELQSLRR 248

RESULT 48
 ID 09FPKO PRELIMINARY; PRT: 326 AA.
 AC 09FPKO; 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE AT4938460.
 GN AT4938460/F20M13.20.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shinn P., Chen H., Cheuk R., Kim C.J., Banh J., Bower L.,
 RA Carinici P., Chung M.K., Goldsmith A.D., Hayashizaki Y., Ishida J.,
 RA Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M.,
 RA Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Pham P.K., Quach H.L., Sakano H., Sakurai T., Searou M., Seki M.,
 RA Southwick A., Toriumi M., Yamada K., Yu G., Shinzaki K., Davis R.W.,
 RA Theologis A., Ecker J.R.;
 RT "Arabidopsis cDNA clones."
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF324662; AAC40013.1;
 DR InterPro: IPR000092; Polyprenyl_synth.
 DR Pfam: PF00348; polyprenyl_synth.1.
 DR PROSITE: PS00723; POLYPRENYL_SYNTHET_1; 1.
 SQ SEQUENCE 326 AA; 35246 MW; 894C5A00740CD475 CRC64;

Query Match 2.8%; Score 7; DB 10; Length 326;
 Best Local Similarity 100.0%; Pred. No. 1.le+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 ELQSLRR 60
 |||||
 Db 242 ELQSLRR 248

RESULT 49
 ID 09SZM6 PRELIMINARY; PRT: 326 AA.
 AC 09SZM6; 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Geranylgeranyl pyrophosphate synthase-related protein
 (AT4938460/F20M13.20).
 GN F20M13.20 OR AT4938460.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Medler H., Kutzner M., Wambutt R., Bancroft I., Mewes H.W.,
 RA Meyer K.F.X., Scheller C.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 [2]

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RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RP [3]
RP SEQUENCE FROM N.A.
RA Weiler H., Kutzner M., Wambutt R., Mewes H.W., Lemcke K.,
RA Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Liu S.X., Sakano H., Pham P.K., Yamada K., Banh J., Etgu P., Lee J.M.,
RA Toriumi M., Yu G., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RL "Full Length cDNA of gene F20M13.20/AT4938460 (GI:7270829).";
RN [6]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL "Full Length cDNA of gene F20M13.20/AT4938460 (GI:7270829).";
RN [7]
RP Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RL "Arabidopsis ORF clones.";
RN [9]
RP Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Shinn P., Banh J.,
RA Bowser L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,
RA Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M.,
RA Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K.,
RA Davis R.W., Theologis A., Ecker J.R.;
RL "Arabidopsis cDNA clones.";
RN [11]
RP Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [12]
RP EMBL; AL035540; CAB37502.1; -
DR EMBL; AL161593; CAB80510.1; -
DR EMBL; AF326906; AAG41488.1; -
DR EMBL; AF339725; AAK00407.1; -
DR EMBL; AY057734; AAL15364.1; -
DR EMBL; AF372915; AAK49631.1; -
DR InterPro; IPR000092; PolyPrenyl_syn; 1.
DR Pfam; PF00348; PolyPrenyl_syn; 1.
DR PROSITE; PS00723; POLYPRENYL_SYNTHET_1; 1.
SQ SEQUENCE 326 AA; 35188 MW; 89494E0740CD475 CRC64;

Query Match 2.8%; Score 7; DB 10; Length 326;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 54 ELOSRLR 60
| | | | |
Db 242 ELOSRLR 248

RESULT 50

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O9XEU4
ID O9XEU4 PRELIMINARY; PRT; 331 AA.
AC O9XEU4;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE Putative reverse transcriptase.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Euphorbia; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Liaca V., Lou A., Young S., Messing J.;
RL "Microsytamy in a gene-dense region in maize, sorghum, and rice.";
RN [2]
DR EMBL; AF119222; AAD27672.1; -
KW RNA-directed DNA polymerase.
SQ SEQUENCE 331 AA; 37867 MW; BA451072D5D8BD0C CRC64;

Query Match 2.8%; Score 7; DB 10; Length 311;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 52 QTELQSL 58
| | | | |
Db 121 QTELQSL 127

RESULT 51
O68405
ID O68405 PRELIMINARY; PRT; 336 AA.
AC O68405;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE Orf UL151.
OS Human cytomegalovirus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10359;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=TOLEDO;
RC MEDLINE=96099416; PubMed=8523595;
RA Cha T.A., Tom E., Kemble G.W., Duke G.M., Mocarski E.S., Spaete R.R.;
RT "Human cytomegalovirus clinical isolates carry at least 19 genes not
found in laboratory strains.";
RL J. Virol. 70:78-83(1996).
DR EMBL; U33331; AAA85892.1; -
SQ SEQUENCE 336 AA; 35116 MW; 9F865E5019F69D0C CRC64;

Query Match 2.8%; Score 7; DB 12; Length 336;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 142 LRRGRGL 148
| | | | |
Db 82 LRRGRGL 88

RESULT 52
O9FLV7
ID O9FLV7 PRELIMINARY; PRT; 349 AA.
AC O9FLV7;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE Genomic DNA, chromosome 5, p1 clone:MZP18.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

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OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
 ON NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=98290546; PubMed=9629582;
 RA Sato S., Kaneo T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,
 Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. IV.
 RT Sequence features of the regions of 1,456,315 bp covered by nineteen
 RT physically assigned P1 and TAC clones.";
 RL DNA Res 5:41-54(1998)
 DR EMBL; AB009056; BAB08728.1; -
 SQ SEQUENCE 349 AA; 39783 MW; 33F598698FB1CC9 CRC64;
 Query Match 2.8%; Score 7; DB 10; Length 349;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

100 SRKRRV 106
 |||||
 169 SRKRRV 175

RESULT 53
 ID 09HLO5 PRELIMINARY; PRT; 353 AA.
 AC 09HLO5;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Hemlin permease (hem) related protein.
 GN TA0172.
 OS Thermoplasma acidophilum.
 OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
 OC Thermoplasmataceae; Thermoplasma.
 ON NCBI_TaxID=2303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 1728;
 RX MEDLINE=20479972; PubMed=11029001;
 RA Ruepp A., Grent W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
 Mewes H.-W., Fishman D., Stocker S., Lupas A.N., Baumeister W.;
 RT "The genome sequence of the thermophilic scavenger Thermoplasma
 RT acidophilum.";
 RL Nature 407:508-513(2000).
 DR EMBL; ALA45063; CAC11318.1; -
 DR InterPro; IPR000522; FeCD; 1.
 DR Pfam; PF01032; FeCD; 1.
 DR ProDom; PD001557; FeCD; 1.
 KM Complete proteome.
 SQ SEQUENCE 353 AA; 37885 MW; 1D04DC507D2DA4BC CRC64;
 Query Match 2.8%; Score 7; DB 17; Length 353;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 GAAAGV 42
 |||||
 DB 116 GAAAGV 122

RESULT 54
 ID 097C19 PRELIMINARY; PRT; 354 AA.
 AC 097C19;
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Iron III diclrate transport system permease protein.
 GN TV0286 OR TV0286872.
 OS Thermoplasma volcanium.
 OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;

OC Thermoplasmataceae; Thermoplasma.
 ON NCBI_TaxID=50339;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GSS1 / DSM 4299 / JCM 9571;
 RX MEDLINE=20570466; PubMed=11121031;
 RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
 RA Kawashima T., Yamamoto Y., Watanabe K., Yamazaki M., Kaneshiro K., Kawamoto T.,
 RA Nishihara T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
 RT "Archaeal adaptation to higher temperatures revealed by genomic
 RT sequence of Thermoplasma volcanium.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
 DR EMBL; AP000991; BAB59428.1; -
 DR InterPro; IPR000522; FeCD.
 DR Pfam; PF01032; FeCD; 1.
 DR ProDom; PD001557; FeCD; 1.
 KM Complete proteome.
 SQ SEQUENCE 354 AA; 38220 MW; 5347A99FFD3D588-CRC64;
 Query Match 2.8%; Score 7; DB 17; Length 354;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 GAAAGV 42
 |||||
 DB 117 GAAAGV 123

RESULT 55
 ID Q20880 PRELIMINARY; PRT; 359 AA.
 AC Q20880;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE F56D5.1 protein.
 GN F56D5.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 ON NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Matthews P.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C. elegans: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL; Z69662; CA93499.1; -
 DR InterPro; IPR000087; Collagen.
 DR InterPro; IPR002486; COL cuticle_N.
 DR Pfam; PF01391; Collagen; 2.
 DR Pfam; PF01484; COL cuticle_N; 1.
 SQ SEQUENCE 359 AA; 36515 MW; 1F66C351DC24770D CRC64;
 Query Match 2.8%; Score 7; DB 5; Length 359;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PKGPPN 17
 |||||
 DB 221 PKGPPN 227

RESULT 56
 ID 09LRX6 PRELIMINARY; PRT; 359 AA.
 AC 09LRX6;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE Similarity to HEP1 protein from Anabaena PCC7120.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustrods II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=20277480; PubMed=10819329;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
 features of the regions of 4,504,864 bp covered by sixty P1 and TAC
 clones."
 DN DNA Ref. 7:131-135(2000).
 DR EMBL: AB028609; BAB02895.1;
 SO SEQUENCE 359 AA; 40668 MW; C6042D199BBE3FD CRC64;
 Query Match 2.8%; Score 7; DB 10; Length 359;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 100 SRKRAV 106
 |||||
 DB 179 SRKRAV 185

RESULT 57
 ID 068551 PRELIMINARY; PRT; 360 AA.
 AC 068551;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Triacylglycerol lipase (EC 3.1.1.3).
 OS Pseudomonas luteola.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OC NCBI_TaxID=47886;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Litchner D., Ginster A., Skein E.;
 RT Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF050153; AAC05510.1; -
 DR HSSP; P22088; 31IP.
 DR InterPro; IPR000073; Abhydrolase.
 DR InterPro; IPR000734; Lipase.
 DR InterPro; IPR000379; Ser_estere_site.
 DR Pfam; PF00561; abhydrolase.1.
 DR PROSITE; PS00120; LIPASE_SER; 1.
 KW Hydrolase.
 SO SEQUENCE 360 AA; 37189 MW; BD0806C22D58AFB0 CRC64;
 Query Match 2.8%; Score 7; DB 2; Length 360;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 40 GAVACAM 46
 |||||
 DB 8 GAVACAM 14

RESULT 58
 ID 09NOR7 PRELIMINARY; PRT; 378 AA.
 AC 09NOR7;
 ID 09NOR7;

DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE Interphoreceptor retinoid binding protein (Fragment).
 OS IRBP.
 OS Thyliams pallidior (pallid fat-tailed opossum).
 OC Eukaryota; Metazoa; Chordata; Cranista; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Thyliams.
 OC NCBI_TaxID=126301;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jansa S.A., Voss R.S.;
 RT "Phylogenetic studies on didelphid marsupials I. Introduction and
 preliminary results from nuclear IRBP gene sequences."
 RL J. Mammal. Evol. 7:43-77(2000).
 DR EMBL: AF257689; AAF72016.1; -
 DR InterPro; IPR003581; TSpc.
 DR Pfam; PF02692; IRBP; 1.
 DR SMART; SM00245; TSpc; 1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 378
 SO SEQUENCE 378 AA; 41175 MW; 3BE299E78D586558 CRC64;
 Query Match 2.8%; Score 7; DB 6; Length 378;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 219 LHOGDIL 225
 |||||
 DB 133 LHOGDIL 139

RESULT 59
 ID 09NOSO PRELIMINARY; PRT; 379 AA.
 AC 09NOSO;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE Interphoreceptor retinoid binding protein (Fragment).
 OS IRBP.
 OS Gracilinanus microtarsus (Brazilian gracile mouse opossum).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Gracilinanus.
 OC NCBI_TaxID=126289;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jansa S.A., Voss R.S.;
 RT "Phylogenetic studies on didelphid marsupials I. Introduction and
 preliminary results from nuclear IRBP gene sequences."
 RL J. Mammal. Evol. 7:43-77(2000).
 DR EMBL: AF257686; AAF72013.1; -
 DR InterPro; IPR003581; TSpc.
 DR Pfam; PF02692; IRBP; 1.
 DR SMART; SM00245; TSpc; 1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 379
 SO SEQUENCE 379 AA; 41197 MW; C6A8B0248D068FB0 CRC64;
 Query Match 2.8%; Score 7; DB 6; Length 379;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 219 LHOGDIL 225
 |||||
 DB 134 LHOGDIL 140

RESULT 60
 ID 09LV20 PRELIMINARY; PRT; 383 AA.
 ID 09LV20

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AC 09UV20.
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Nodulin-like protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Nakamura Y.;
RL MEDLINE=20363099; PubMed=10907853;
"Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the regions of 4,251,695 bp covered by ninety pl.
TAC and BAC clones.";
RT DNA Res. 7:217-221(2000).
DR EMBL; AB020749; BAB02033.1; -.
DR InterPro; IPR000620; DUF6.
DR Pfam; PF00892; DUF6. 2.
SQ SEQUENCE 383 AA; 42845 MW; E014B3128B3FB517 CRC64;

Query Match 2.8%; Score 7; DB 10; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 99 RSRKRA 105
DB 11 RSRKRA 17

RESULT 61
Q9N0R9 PRELIMINARY; PRT; 385 AA.
AC Q9N0R9;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Interphoreceptor retinoid binding protein (Fragment).
GN IRBP.
OS Gracilinanus microcarus (Brazilian gracile mouse opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Gracilinanus.
OC NCBI_TaxID=126289;
RN [1]
RP SEQUENCE FROM N.A.
RA Jansa S.A., Voss R.S.;
RT "Phylogenetic studies on didelphid marsupials I. Introduction and
preliminary results from nuclear IRBP gene sequences.";
RL J. Mammal. Evol. 7:43-77(2000).
DR EMBL; AF257687; AAF72014.1; -.
DR InterPro; IPR003581; TSPC.
DR Pfam; PF02692; IRBP. 1.
DR SMART; SM00245; TSPC. 1.
KW Receptor.
FT NON_TER 1
FT SEQUENCE 385 AA; 41973 MW; E2C0E0A4E7B05322 CRC64;

Query Match 2.8%; Score 7; DB 6; Length 385;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 LHQGDIL 225
DB 140 LHQGDIL 146
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RESULT 62
Q9MYN9 PRELIMINARY; PRT; 386 AA.
AC Q9MYN9;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Interphoreceptor retinoid binding protein (Fragment).
GN IRBP.
OS Marmosops impavidus (Andean slender mouse opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Marmosops.
OC NCBI_TaxID=42722;
RN [1]
RP SEQUENCE FROM N.A.
RA Jansa S.A., Voss R.S.;
RT "Phylogenetic studies on didelphid marsupials I. Introduction and
preliminary results from nuclear IRBP gene sequences.";
RL J. Mammal. Evol. 7:43-77(2000).
DR EMBL; AF257698; AAF72025.1; -.
DR EMBL; AF257695; AAF72022.1; -.
DR InterPro; IPR003581; TSPC.
DR Pfam; PF02692; IRBP. 1.
DR SMART; SM00245; TSPC. 1.
KW Receptor.
FT NON_TER 1
FT SEQUENCE 386 AA; 42147 MW; 316E953086E4E3 CRC64;

Query Match 2.8%; Score 7; DB 6; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 LHQGDIL 225
DB 141 LHQGDIL 147

RESULT 63
Q9MYN7 PRELIMINARY; PRT; 386 AA.
AC Q9MYN7;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Interphoreceptor retinoid binding protein (Fragment).
GN IRBP.
OS Marmosops parvidens (delicate slender mouse opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Marmosops.
OC NCBI_TaxID=126298;
RN [1]
RP SEQUENCE FROM N.A.
RA Jansa S.A., Voss R.S.;
RT "Phylogenetic studies on didelphid marsupials I. Introduction and
preliminary results from nuclear IRBP gene sequences.";
RL J. Mammal. Evol. 7:43-77(2000).
DR EMBL; AF257680; AAF72007.1; -.
DR EMBL; AF257677; AAF72004.1; -.
DR InterPro; IPR003581; TSPC.
DR Pfam; PF02692; IRBP. 1.
DR SMART; SM00245; TSPC. 1.
KW Receptor.
FT NON_TER 1
FT SEQUENCE 386 AA; 42087 MW; 3530F20B3A0D96DB CRC64;

Query Match 2.8%; Score 7; DB 6; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 219 LHOGDIL 225
|||||
Db 141 LHOGDIL 147

RESULT 64

Q9MYM9 PRELIMINARY; PRT; 386 AA.
ID Q9MYM9
AC Q9MYM9;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Interphotoreceptor retinoid binding protein (Fragment).
GN IRBP.
OS Didelphis marsupialis (Southern opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9268;
RN [1]
RP SEQUENCE FROM N.A.
RA Jansa S.A., Voss R.S.;
RT "Phylogenetic studies on didelphid marsupials I. Introduction and preliminary results from nuclear IRBP gene sequences.";
RL J. Mammal. Evol. 7:43-77(2000).
DR EMBL; AF257708; AAF72035.1; -.
DR EMBL; AF257703; AAF72030.1; -.
DR InterPro; IPR003581; TSPC.
DR Pfam; PF02692; IRBP; 1.
DR SMART; SM00245; TSPC; 1.
KW Receptor.
FT NON_TER 1 386
FT NON_TER 1 386
SQ SEQUENCE 386 AA; 42086 MW; 70EDFF45D9AAB69 CRC64;

Query Match 2.8%; Score 7; DB 6; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 219 LHOGDIL 225
|||||
Db 141 LHOGDIL 147

RESULT 65

Q9MYM3 PRELIMINARY; PRT; 386 AA.
ID Q9MYM3
AC Q9MYM3;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Interphotoreceptor retinoid binding protein (Fragment).
GN IRBP.
OS Marmosops noctivagus (white-bellied slender mouse opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Marmosops.
OX NCBI_TaxID=126296;
RN [1]
RP SEQUENCE FROM N.A.
RA Jansa S.A., Voss R.S.;
RT "Phylogenetic studies on didelphid marsupials I. Introduction and preliminary results from nuclear IRBP gene sequences.";
RL J. Mammal. Evol. 7:43-77(2000).
DR EMBL; AF257704; AAF72031.1; -.
DR EMBL; AF257696; AAF72023.1; -.
DR InterPro; IPR003581; TSPC.
DR Pfam; PF02692; IRBP; 1.
DR SMART; SM00245; TSPC; 1.
KW Receptor.
FT NON_TER 1 386
FT NON_TER 1 386
SQ SEQUENCE 386 AA; 42061 MW; C14C953095369F70 CRC64;

Query Match 2.8%; Score 7; DB 6; Length 386;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 219 LHOGDIL 225
|||||
Db 141 LHOGDIL 147

RESULT 66

Q9N0S9 PRELIMINARY; PRT; 386 AA.
ID Q9N0S9
AC Q9N0S9;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Interphotoreceptor retinoid binding protein (Fragment).
GN IRBP.
OS Caluromysiaops irrupta (black-shouldered opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Caluromysiaops.
OX NCBI_TaxID=126286;
RN [1]
RP SEQUENCE FROM N.A.
RA Jansa S.A., Voss R.S.;
RT "Phylogenetic studies on didelphid marsupials I. Introduction and preliminary results from nuclear IRBP gene sequences.";
RL J. Mammal. Evol. 7:43-77(2000).
DR EMBL; AF257675; AAF72002.1; -.
DR InterPro; IPR003581; TSPC.
DR Pfam; PF02692; IRBP; 1.
DR SMART; SM00245; TSPC; 1.
KW Receptor.
FT NON_TER 1 386
FT NON_TER 1 386
SQ SEQUENCE 386 AA; 42106 MW; BF2B256F970FC1AC CRC64;

Query Match 2.8%; Score 7; DB 6; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 219 LHOGDIL 225
|||||
Db 141 LHOGDIL 147

RESULT 67

Q9N0S8 PRELIMINARY; PRT; 386 AA.
ID Q9N0S8
AC Q9N0S8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Interphotoreceptor retinoid binding protein (Fragment).
GN IRBP.
OS Marmosops noctivagus (white-bellied slender mouse opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Marmosops.
OX NCBI_TaxID=126296;
RN [1]
RP SEQUENCE FROM N.A.
RA Jansa S.A., Voss R.S.;
RT "Phylogenetic studies on didelphid marsupials I. Introduction and preliminary results from nuclear IRBP gene sequences.";
RL J. Mammal. Evol. 7:43-77(2000).
DR EMBL; AF257676; AAF72003.1; -.
DR InterPro; IPR003581; TSPC.
DR Pfam; PF02692; IRBP; 1.
DR SMART; SM00245; TSPC; 1.
KW Receptor.
FT NON_TER 1 386
FT NON_TER 1 386
SQ SEQUENCE 386 AA; 42008 MW; 351DC4758E37346A CRC64;

Query Match 2.8%; Score 7; DB 6; Length 386;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 LHOGDIL 225
 |||||
 Db 141 LHOGDIL 147

RESULT 68

Q9N0S7 PRELIMINARY; PRT; 386 AA.
 AC Q9N0S7;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE Interphoreceptor retinoid binding protein (Fragment).
 GN IRBP.
 OS Didelphis marsupialis virginiana (North American opossum).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
 NCBI_TaxID=9267;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jansa S.A., Voss R.S.;
 RT "Phylogenetic studies on didelphid marsupials I. Introduction and preliminary results from nuclear IRBP gene sequences.";
 RL J. Mammal. Evol. 7:43-77(2000).
 DR EMBL; AF257678; AAF72005.1; -.
 DR InterPro; IPR003581; TSPC.
 DR Pfam; PF02692; IRBP; 1.
 DR SMART; SM00245; TSPC; 1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 386
 SQ SEQUENCE 386 AA; 42197 MW; 121FCE422750DC91 CRC64;

Query Match 2.8%; Score 7; DB 6; Length 386;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 LHOGDIL 225
 |||||
 Db 141 LHOGDIL 147

RESULT 69

Q9N0S6 PRELIMINARY; PRT; 386 AA.
 AC Q9N0S6;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE Interphoreceptor retinoid binding protein (Fragment).
 GN IRBP.
 OS Chironectes minimus (water opossum).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Metatheria; Didelphimorphia; Didelphidae; Chironectes.
 NCBI_TaxID=91500;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jansa S.A., Voss R.S.;
 RT "Phylogenetic studies on didelphid marsupials I. Introduction and preliminary results from nuclear IRBP gene sequences.";
 RL J. Mammal. Evol. 7:43-77(2000).
 DR EMBL; AF257679; AAF72006.1; -.
 DR InterPro; IPR003581; TSPC.
 DR Pfam; PF02692; IRBP; 1.
 DR SMART; SM00245; TSPC; 1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 386
 SQ SEQUENCE 386 AA; 42169 MW; 3D026D50038CF12A CRC64;

Query Match 2.8%; Score 7; DB 6; Length 386;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 LHOGDIL 225
 |||||
 Db 141 LHOGDIL 147

RESULT 70

Q9N0S5 PRELIMINARY; PRT; 386 AA.
 AC Q9N0S5;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE Interphoreceptor retinoid binding protein (Fragment).
 GN IRBP.
 OS Marmosa lepida (little rufous mouse opossum).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Metatheria; Didelphimorphia; Didelphidae; Marmosa.
 NCBI_TaxID=126294;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jansa S.A., Voss R.S.;
 RT "Phylogenetic studies on didelphid marsupials I. Introduction and preliminary results from nuclear IRBP gene sequences.";
 RL J. Mammal. Evol. 7:43-77(2000).
 DR EMBL; AF257681; AAF72008.1; -.
 DR InterPro; IPR003581; TSPC.
 DR Pfam; PF02692; IRBP; 1.
 DR SMART; SM00245; TSPC; 1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 386
 SQ SEQUENCE 386 AA; 42118 MW; A5628DBF1626240B CRC64;

Query Match 2.8%; Score 7; DB 6; Length 386;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 LHOGDIL 225
 |||||
 Db 141 LHOGDIL 147

RESULT 71

Q9N0S4 PRELIMINARY; PRT; 386 AA.
 AC Q9N0S4;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE Interphoreceptor retinoid binding protein (Fragment).
 GN IRBP.
 OS Didelphis albiventris (white-eared opossum).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
 NCBI_TaxID=42716;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jansa S.A., Voss R.S.;
 RT "Phylogenetic studies on didelphid marsupials I. Introduction and preliminary results from nuclear IRBP gene sequences.";
 RL J. Mammal. Evol. 7:43-77(2000).
 DR EMBL; AF257682; AAF72009.1; -.
 DR InterPro; IPR003581; TSPC.
 DR Pfam; PF02692; IRBP; 1.
 DR SMART; SM00245; TSPC; 1.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 386

SEQ SEQUENCE 386 AA; 42221 MW; 4B5F5B629CA2B62D CRC64;

Query Match 2.8%; Score 7; DB 6; Length 386;

Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 219 LHOGDIL 225

Db 141 LHOGDIL 147

RESULT 72

Q9N0S3 PRELIMINARY; PRT; 386 AA.

AC Q9N0S3; 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DE Interphoreceptor retinoid binding protein (Fragment).

OS Didelphis albiventris (white-eared opossum).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.

OC NCBI_TaxID=42716;

RP SEQUENCE FROM N.A.

RA Jansa S.A., Voss R.S.;

RT "Phylogenetic studies on didelphid marsupials I. Introduction and

RL J. Mammal. Evol. 7:43-77(2000).

DR EMBL; AF257683; AAF72010.1; -.

DR InterPro; IPR003581; TSPC.

DR Pfam; PF02692; IRBP; 1.

DR SMART; SM00245; TSPC; 1.

FT NON_TER 1

FT NON_TER 386

SEQ SEQUENCE 386 AA; 42227 MW; 2D624B6E31CC906 CRC64;

Query Match 2.8%; Score 7; DB 6; Length 386;

Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 219 LHOGDIL 225

Db 141 LHOGDIL 147

SULT 73

Q9N0S2 PRELIMINARY; PRT; 386 AA.

AC Q9N0S2; 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DE Interphoreceptor retinoid binding protein (Fragment).

OS Euteleostomi; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.

OC NCBI_TaxID=42716;

RP SEQUENCE FROM N.A.

RA Jansa S.A., Voss R.S.;

RT "Phylogenetic studies on didelphid marsupials I. Introduction and

RL J. Mammal. Evol. 7:43-77(2000).

DR EMBL; AF257684; AAF72011.1; -.

DR InterPro; IPR003581; TSPC.

DR Pfam; PF02692; IRBP; 1.

DR SMART; SM00245; TSPC; 1.

FT NON_TER 1

FT NON_TER 386

SEQ SEQUENCE 386 AA; 42227 MW; 2D624B6E31CC906 CRC64;

Query Match 2.8%; Score 7; DB 6; Length 386;

Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 219 LHOGDIL 225

Db 141 LHOGDIL 147

FT NON_TER 386 386

SEQ SEQUENCE 386 AA; 42170 MW; 0C839B3F830C8AFD CRC64;

Query Match 2.8%; Score 7; DB 6; Length 386;

Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 219 LHOGDIL 225

Db 141 LHOGDIL 147

RESULT 74

Q9N0R8 PRELIMINARY; PRT; 386 AA.

AC Q9N0R8; 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DE Interphoreceptor retinoid binding protein (Fragment).

OS Glironia venusta (bushy-tailed opossum).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Glironia.

OC NCBI_TaxID=42715;

RP SEQUENCE FROM N.A.

RA Jansa S.A., Voss R.S.;

RT "Phylogenetic studies on didelphid marsupials I. Introduction and

RL J. Mammal. Evol. 7:43-77(2000).

DR EMBL; AF257688; AAF72015.1; -.

DR InterPro; IPR003581; TSPC.

DR Pfam; PF02692; IRBP; 1.

DR SMART; SM00245; TSPC; 1.

FT NON_TER 1

FT NON_TER 386

SEQ SEQUENCE 386 AA; 42040 MW; 9A0919B68FE48926 CRC64;

Query Match 2.8%; Score 7; DB 6; Length 386;

Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 219 LHOGDIL 225

Db 141 LHOGDIL 147

RESULT 75

Q9N0R6 PRELIMINARY; PRT; 386 AA.

AC Q9N0R6; 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DE Interphoreceptor retinoid binding protein (Fragment).

OS Caluromys lanatus (western woolly opossum).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Caluromys.

OC NCBI_TaxID=42713;

RP SEQUENCE FROM N.A.

RA Jansa S.A., Voss R.S.;

RT "Phylogenetic studies on didelphid marsupials I. Introduction and

RL J. Mammal. Evol. 7:43-77(2000).

DR EMBL; AF257690; AAF72017.1; -.

DR InterPro; IPR003581; TSPC.

DR Pfam; PF02692; IRBP; 1.

DR SMART; SM00245; TSPC; 1.

FT NON_TER 1

FT NON_TER 386

SEQ SEQUENCE 386 AA; 42040 MW; 9A0919B68FE48926 CRC64;

Query Match 2.8%; Score 7; DB 6; Length 386;

Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 219 LHOGDIL 225

Db 141 LHOGDIL 147

4

FT NON_TER 1 1
FT NON_TER 386 386
SQ SEQUENCE 386 AA; 42178 MW; CGB9CF814D386624 CRC64;

Query Match 2.8%; Score 7; DB 6; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 219 LHQGDIL 225
|||
|||
Db 141 LHQGDIL 147

Search completed: March 26, 2003, 07:48:42
Job time : 96 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 07:31:11 ; Search time 15 Seconds
(without alignments)
490.382 Million cell updates/sec

Title: US-09-724-341-8
Perfect score: 1304
Sequence: 1 MPASSPFLAPKGPVREPALSVLWLSGALGAVACAMLLTQOTELQSLRR 250

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues
al number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1304	100.0	250	4	US-08-883-086-2 Sequence 2, Appl
2	1296	99.4	250	4	US-09-153-927-4 Sequence 4, Appl
3	1285	98.5	247	4	US-09-157-864-4 Sequence 4, Appl
4	1195	91.6	234	4	US-09-157-864-2 Sequence 2, Appl
5	1031	79.1	205	4	US-09-286-529-5 Sequence 5, Appl
6	762	58.4	147	4	US-08-883-086-3 Sequence 3, Appl
7	710	54.4	136	4	US-09-589-287B-20 Sequence 20, Appl
8	244.5	18.8	285	4	US-09-286-529-1 Sequence 1, Appl
9	244.5	18.8	285	4	US-09-589-287B-2 Sequence 2, Appl
10	232	17.8	266	4	US-09-589-287B-19 Sequence 19, Appl
11	231.5	17.8	219	4	US-09-589-287B-28 Sequence 28, Appl
12	227.5	17.4	219	4	US-09-589-287B-30 Sequence 30, Appl
13	210.5	16.1	289	4	US-09-589-287B-38 Sequence 38, Appl
14	210	16.1	145	4	US-09-286-529-21 Sequence 21, Appl
15	208	16.0	155	4	US-09-589-287B-23 Sequence 23, Appl
16	131	10.0	391	4	US-09-342-681C-2 Sequence 2, Appl
17	122	9.4	24	4	US-09-157-864-6 Sequence 6, Appl
18	112.5	8.6	155	1	US-07-994-469A-80 Sequence 80, Appl
19	110	8.4	377	4	US-09-342-681C-4 Sequence 4, Appl
20	108.5	8.3	155	1	US-07-994-469A-77 Sequence 77, Appl
21	108.5	8.3	155	1	US-07-994-469A-79 Sequence 79, Appl
22	107.5	8.2	155	1	US-07-994-469A-45 Sequence 45, Appl
23	107.5	8.2	155	1	US-07-994-469A-67 Sequence 67, Appl
24	107.5	8.2	155	1	US-07-994-469A-76 Sequence 76, Appl
25	107.5	8.2	155	1	US-07-994-469A-78 Sequence 78, Appl
26	107	8.2	154	1	US-07-994-469A-75 Sequence 75, Appl
27	106.5	8.2	158	1	US-07-994-469A-86 Sequence 86, Appl

28	106.5	8.2	158	6	5182196-2	Patent No. 5182196
29	106.5	8.2	161	1	US-07-994-469A-61	Sequence 61, Appl
30	106.5	8.2	163	1	US-07-994-469A-64	Sequence 64, Appl
31	105.5	8.1	150	1	US-07-668-517-13	Sequence 13, Appl
32	105.5	8.1	151	1	US-07-668-517-27	Sequence 27, Appl
33	105.5	8.1	158	1	US-07-994-469A-52	Sequence 52, Appl
34	105.5	8.1	176	6	5180811-12	Sequence 12, Appl
35	103.5	7.9	145	1	US-07-994-469A-9	Patent No. 5180811
36	103.5	7.9	155	1	US-07-994-469A-50	Sequence 9, Appl
37	103.5	7.9	155	1	US-07-994-469A-68	Sequence 50, Appl
38	103.5	7.9	157	1	US-07-668-517-33	Sequence 68, Appl
39	103.5	7.9	157	1	US-07-794-400-1	Sequence 33, Appl
40	103.5	7.9	157	1	US-08-041-648-2	Sequence 2, Appl
41	103.5	7.9	157	1	US-07-940-605A-5	Sequence 1, Appl
42	103.5	7.9	157	1	US-08-107-235-1	Sequence 5, Appl
43	103.5	7.9	157	1	US-08-217-529-2	Sequence 2, Appl
44	103.5	7.9	157	1	US-08-318-193-86	Sequence 86, Appl
45	103.5	7.9	157	1	US-08-397-470-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-883-086-2
; Sequence 2, Application US/08883086
; Patent No. 6171787
; GENERAL INFORMATION:
; APPLICANT: WILEY, STEVEN
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF INVENTION: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,086
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Potembski, Priscilla E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 6134.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-937-0378
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6171787e
; US-08-883-086-2
Query Match 100.0%; Score 1304; DB 4; Length 250;
Best Local Similarity 100.0%; Pred No. 7.4e-133;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPASSPFLAPKGPVREPALSVLWLSGALGAVACAMLLTQOTELQSLRR 60

Db 1 MPASSPFLAPKPGPNMGPFVREBPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60
Qy 61 EVSRLQGTGPGSPQNGEGYPMQSLPEQSSDLEAMENGERSRKRRAVLTOKOKHSHVHL 120
Db 61 EVSRLQGTGPGSPQNGEGYPMQSLPEQSSDLEAMENGERSRKRRAVLTOKOKHSHVHL 120
Qy 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYGVRIODAGVYLLYSQVLFDVFTMGQ 180
Db 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYGVRIODAGVYLLYSQVLFDVFTMGQ 180
Qy 181 VVSREGGROETLFRICRSMPSHPDRAVNSCYSGAVFHLHOGDILSVIIPRAKATLNSP 240
Db 181 VVSREGGROETLFRICRSMPSHPDRAVNSCYSGAVFHLHOGDILSVIIPRAKATLNSP 240
Qy 241 HGTFLGFVKL 250
Db 241 HGTFLGFVKL 250

ULT 2

US-09-153-927-4

Sequence 4, Application US/09153927A
Patent No. 6297022
GENERAL INFORMATION:
APPLICANT: McDonnell, Peter C.
APPLICANT: Young, Peter R.
APPLICANT: Zou, Jun
TITLE OF INVENTION: A Method of Identifying Agonists and
TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3
FILE REFERENCE: GH50031
CURRENT FILING DATE: 1998-09-16
EARLIER APPLICATION NUMBER: 60/061,334
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 250
TYPE: PRT
ORGANISM: Human
US-09-153-927-4

No more found

Query Match 99.4%; Score 1296; DB 4; Length 250;
Best Local Similarity 99.6%; Pred. No. 5,4e-133;
Matches 249; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 MPASSPFLAPKPGPNMGPFVREBPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60
Qy 61 EVSRLQGTGPGSPQNGEGYPMQSLPEQSSDLEAMENGERSRKRRAVLTOKOKHSHVHL 120
Db 61 EVSRLQGTGPGSPQNGEGYPMQSLPEQSSDLEAMENGERSRKRRAVLTOKOKHSHVHL 120
Qy 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYGVRIODAGVYLLYSQVLFDVFTMGQ 180
Db 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYGVRIODAGVYLLYSQVLFDVFTMGQ 180
Qy 181 VVSREGGROETLFRICRSMPSHPDRAVNSCYSGAVFHLHOGDILSVIIPRAKATLNSP 240
Db 181 VVSREGGROETLFRICRSMPSHPDRAVNSCYSGAVFHLHOGDILSVIIPRAKATLNSP 240
Qy 241 HGTFLGFVKL 250
Db 241 HGTFLGFVKL 250

RESULT 3
US-09-157-864-4
Sequence 4, Application US/09157864
Patent No. 6440694

GENERAL INFORMATION:
APPLICANT: Bienkowski, Michael J
APPLICANT: Mills, Cynthia J
APPLICANT: Jones, David A
TITLE OF INVENTION: TNF-Related Death Ligand
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
ADDRESSEE: Legal Services
STREET: 301 Henrietta Street
CITY: Kalamazoo
STATE: MI
COUNTRY: USA
ZIP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/157,864
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kerber, Lori L.
REGISTRATION NUMBER: 41,113
REFERENCE//DOCKET NUMBER: 6111.N CN1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616/833-0974
TELEFAX: 616/833-8897
TELEX: 224401
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-157-864-4

Query Match 98.5%; Score 1285; DB 4; Length 247;
Best Local Similarity 100.0%; Pred. No. 8,2e-131;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPASSPFLAPKPGPNMGPFVREBPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60
Db 1 MPASSPFLAPKPGPNMGPFVREBPALSVLWLSWGALGAVACAMALLTQOTELQSLRR 60
Qy 61 EVSRLQGTGPGSPQNGEGYPMQSLPEQSSDLEAMENGERSRKRRAVLTOKOKHSHVHL 120
Db 61 EVSRLQGTGPGSPQNGEGYPMQSLPEQSSDLEAMENGERSRKRRAVLTOKOKHSHVHL 120
Qy 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYGVRIODAGVYLLYSQVLFDVFTMGQ 180
Db 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYGVRIODAGVYLLYSQVLFDVFTMGQ 180
Qy 181 VVSREGGROETLFRICRSMPSHPDRAVNSCYSGAVFHLHOGDILSVIIPRAKATLNSP 240
Db 181 VVSREGGROETLFRICRSMPSHPDRAVNSCYSGAVFHLHOGDILSVIIPRAKATLNSP 240
Qy 241 HGTFLG 246
Db 241 HGTFLG 246

RESULT 4
US-09-157-864-2
Sequence 2, Application US/09157864
Patent No. 6440694
GENERAL INFORMATION:
APPLICANT: Bienkowski, Michael J
APPLICANT: Mills, Cynthia J
APPLICANT: Jones, David A

TITLE OF INVENTION: TNF-Related Death Ligand
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
ADDRESSEE: Legal Services
STREET: 301 Henrietta Street
CITY: Kalamazoo
STATE: MI
COUNTRY: USA
ZIP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/157,864
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Keither, Lori L.
REGISTRATION NUMBER: 41,113
REFERENCE/DOCKET NUMBER: 6111.N CN1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616/833-0974
TELEFAX: 616/833-8897
TELEX: 224401
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-157-864-2

Query Match 91.6%; Score 1195; DB 4; Length 234;
Best Local Similarity 92.8%; Pred. No. 4e-121;
Matches 232; Conservative 2; Mismatches 0; Indels 16; Gaps 1;

QY 1 MPASSPFLARPKPPGNMGPPVREPALVALWLSGALGAVACAMALLTQTELOSIR 60
DB 1 MPASSPFLARPKPPGNMGPPVREPALVALWLSGALGAVACAMALLTQTELOSIR 60
QY 61 EVSRLOGTGSPSONGEGYPMOSLPQSSDALWAMNGERSRKRRAVLTKOKHSHVHL 120
DB 61 EVSRLOGTGSPSONGEGYPMOSLPQSSDALWAMNGERSRKRRAVLTKOKHSHVHL 120
QY 121 VPINATSKDSDVTEVMMQPALRRGRGLQAGYGVRIODAGVYLLYSQVLFQDVTFTWGQ 180
DB 121 VPINATSKDSDVTEVMMQPALRRGRGLQAGYGVRIODAGVYLLYSQVLFQDVTFTWGQ 180
QY 181 VVSREGGROETLFRICRSMPSHPDRAVNSCYSGVFLHGGDILSVIIPARAKLNISP 240
DB 181 VVSREGGROETLFRICRSMPSHPDRAVNSCYSGVFLHGGDILSVIIPARAKLNISP 240
QY 241 HGTFLGFPVKL 250
DB 241 HGTFLGFPVKL 234

RESULT 5
US-09-286-529-5
Sequence 5, Application US/09286529
Patent No. 6297367
GENERAL INFORMATION:
APPLICANT: Catherine Tribouley
TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
FILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/286,529
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 5
LENGTH: 205
TYPE: PRT
ORGANISM: human
US-09-286-529-5

Query Match 79.1%; Score 1031; DB 4; Length 205;
Best Local Similarity 98.0%; Pred. No. 1.7e-103;
Matches 201; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 46 MALLTQTELOSIRREVSRLOGTGSPSONGEGYPMOSLPQSSDALWAMNGERSRKRRA 105
DB 1 MALLTQTELOSIRREVSRLOGTGSPSONGEGYPMOSLPQSSDALWAMNGERSRKRRA 60
QY 106 VLTKQKQKSHVHLVPINATSKDSDVTEVMMQPALRRGRGLQAGYGVRIODAGVYLL 165
DB 61 VLTKQKQKSHVHLVPINATSKDSDVTEVMMQPALRRGRGLQAGYGVRIODAGVYLL 120
QY 166 YSQVLFQDVTFTWGQVVSREGGROETLFRICRSMPSHPDRAVNSCYSGVFLHGGDIL 225
DB 121 YSQVLFQDVTFTWGQVVSREGGROETLFRICRSMPSHPDRAVNSCYSGVFLHGGDIL 180
QY 226 SVIIPARAKLNISPHTGFLGFPVKL 250
DB 181 SVIIPARAKLNISPHTGFLGFPVKL 205

RESULT 6
US-08-883-086-3
Sequence 3, Application US/08883086
Patent No. 6171787
GENERAL INFORMATION:
APPLICANT: WILEY, STEVEN
TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,086
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Porembski, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 6134.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-0378
TELEFAX: 847-938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 147 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6171787e
US-08-883-086-3

Query Match 58.4%; Score 762; DB 4; Length 147;

Best Local Similarity 100.0%; Pred. No. 1.3e-74;
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 104 RAVLTOKKOKSHVHLVPIINATSKDDSDVTEVMQPALRGRGLQAGGVRIODAGVY 163
Db 1 RAVLTOKKOKSHVHLVPIINATSKDDSDVTEVMQPALRGRGLQAGGVRIODAGVY 60
Oy 164 LLYSOVLFDVYFTMGQVVSREGQROETLFRICIRSMPSHPDRAVNSCYSAVFHLHOGD 223
Db 61 LLYSOVLFDVYFTMGQVVSREGQROETLFRICIRSMPSHPDRAVNSCYSAVFHLHOGD 120
Oy 224 ILTVIIPRAKATLNSPHGTFLGFVKL 250
Db 121 ILTVIIPRAKATLNSPHGTFLGFVKL 147

RESULT 7
US-09-589-287B-20
Sequence 20, Application US/09589287B
Patent No. 6403770

GENERAL INFORMATION:
APPLICANT: Yu et al.
TITLE OF INVENTION: Antibodies to Neutrokin-alpha
FILE REFERENCE: PF343P3C1
CURRENT APPLICATION NUMBER: US/09/589,287B
CURRENT FILING DATE: 2000-06-08
Prior application data removed - check PALM or file wrapper
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 136
TYPE: PRT
ORGANISM: Homo sapiens
US-09-589-287B-20

Query Match 54.4%; Score 710; DB 4; Length 136;
Best Local Similarity 100.0%; Pred. No. 4.6e-69;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 115 HSVLHLPINATSKDDSDVTEVMQPALRGRGLQAGGVRIODAGVYLLYSOVLFDVY 174
Db 1 HSVLHLPINATSKDDSDVTEVMQPALRGRGLQAGGVRIODAGVYLLYSOVLFDVY 60
Oy 175 FTMGQVVSREGQROETLFRICIRSMPSHPDRAVNSCYSAVFHLHOGDILSVIIPARA 234
Db 61 FTMGQVVSREGQROETLFRICIRSMPSHPDRAVNSCYSAVFHLHOGDILSVIIPARA 120
Oy 235 KLNLSPHGTFLGFVKL 250
Db 121 KLNLSPHGTFLGFVKL 136

RESULT 8
US-09-286-529-1
Sequence 1, Application US/09286529
Patent No. 6297367
GENERAL INFORMATION:
APPLICANT: Catherine Tribouley
TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
FILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/286,529
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PasteSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 285
TYPE: PRT
ORGANISM: human
US-09-286-529-1

Query Match 18.8%; Score 244.5; DB 4; Length 285;
Best Local Similarity 29.7%; Pred. No. 2.7e-18;
Matches 70; Conservative 47; Mismatches 90; Indels 29; Gaps 8;

Oy 39 LGAVACAMALLT-----OQTELOSUREVSRLOGTGSPQNGEYFWQSLPEOS--SDA 90
Db 54 LALLSCCLTVVSFYVALAGDLASLRAPLQGHNAEKLPA--GAGAPKAGLEAPAVTAG 111
Oy 91 LEAME-----NGERSRKRRAVLTKOKKOKSHVHLVPIINAT--SKDDSDVTEVMQPA 141
Db 112 LKIFEPAPRAGNSQNSRKRRAVQGFETVTDCLQDLADSETPTIQKSYTFVPMLLS 171
Oy 142 LRRGRGLQAGGVRIODAGVYLLYSOVLFDVYFTMGQVVSRE-----GQGRQETLFR 195
Db 172 FKRGSALEEKENKILVETGYFYIGQVLYTDKTYAMGHILQKXHVFGDELSTVTLFR 231
Oy 196 CIRSNP--SHPDRAVNSCYSAVFHLHOGDILSVIIPRAKATLNSPHGTFLGFVKL 250
Db 232 CIRSNP--SHPDRAVNSCYSAVFHLHOGDILSVIIPRAKATLNSPHGTFLGFVKL 284

RESULT 9
US-09-589-287B-2
Sequence 2, Application US/09589287B
Patent No. 6403770

GENERAL INFORMATION:
APPLICANT: Yu et al.
TITLE OF INVENTION: Antibodies to Neutrokin-alpha
FILE REFERENCE: PF343P3C1
CURRENT APPLICATION NUMBER: US/09/589,287B
CURRENT FILING DATE: 2000-06-08
Prior application data removed - check PALM or file wrapper
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 285
TYPE: PRT
ORGANISM: human
US-09-589-287B-2

Query Match 18.8%; Score 244.5; DB 4; Length 285;
Best Local Similarity 29.7%; Pred. No. 2.7e-18;
Matches 70; Conservative 47; Mismatches 90; Indels 29; Gaps 8;

Oy 39 LGAVACAMALLT-----OQTELOSUREVSRLOGTGSPQNGEYFWQSLPEOS--SDA 90
Db 54 LALLSCCLTVVSFYVALAGDLASLRAPLQGHNAEKLPA--GAGAPKAGLEAPAVTAG 111
Oy 91 LEAME-----NGERSRKRRAVLTKOKKOKSHVHLVPIINAT--SKDDSDVTEVMQPA 141
Db 112 LKIFEPAPRAGNSQNSRKRRAVQGFETVTDCLQDLADSETPTIQKSYTFVPMLLS 171
Oy 142 LRRGRGLQAGGVRIODAGVYLLYSOVLFDVYFTMGQVVSRE-----GQGRQETLFR 195
Db 172 FKRGSALEEKENKILVETGYFYIGQVLYTDKTYAMGHILQKXHVFGDELSTVTLFR 231
Oy 196 CIRSNP--SHPDRAVNSCYSAVFHLHOGDILSVIIPRAKATLNSPHGTFLGFVKL 250
Db 232 CIRSNP--SHPDRAVNSCYSAVFHLHOGDILSVIIPRAKATLNSPHGTFLGFVKL 284

RESULT 10
US-09-589-287B-19
Sequence 19, Application US/09589287B
Patent No. 6403770
GENERAL INFORMATION:
APPLICANT: Yu et al.
TITLE OF INVENTION: Antibodies to Neutrokin-alpha
FILE REFERENCE: PF343P3C1
CURRENT APPLICATION NUMBER: US/09/589,287B
CURRENT FILING DATE: 2000-06-08
Prior application data removed - check PALM or file wrapper
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 266

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-287B-19

Query Match      17.8% Score 232; DB 4; Length 266;
Best Local Similarity 28.5%; Pred. No. 5.6e-17;
Matches 67; Conservative 44; Mismatches 78; Indels 46; Gaps 8;

OY 39 LGAVACAMALLT-----QTELOSRLREVSRLOQTGSPQNGEGYPMQSLPEQS--SDA 90
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 54 LALLSCCLTVSFYQVALAQGLASLRALQGHNAEKLP--GAGAPRAGLEAPAVTAG 111
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 91 LEAME-----NGERSKRAVLTOKOKHSHVLHVPINATSKDSDVTEVMQPAL 142
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 112 LKIEPPAPGEGNSQNSRNKRAV-----QGPEETGSYTFVFWMLLSF 153
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 143 RRGRLAQGYVRIDAGVLLYSQVLFQDVTFTMGVVSRE-----GQGRQETLFR 196
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 154 KRGSALKEKENKILVKEGYFTYQVLTDTKTAMGHILQKKVHVFGDELSTLTLFR 213
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 197 IRSMPSHPDRAVNSCYAGVFHLHQGDILSVIIPRABAKNLSPHGTFLGFVKL 250
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 214 IONMBETLPN---NSCYAGIAKLEEGDELQALIPRENAQISLSDGDVTFPGALKL 265
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 11
US-09-589-287B-28
; Sequence 28, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokine-alpha
; FILE REFERENCE: PF343P3CI
; CURRENT APPLICATION NUMBER: US/09/589,287B
; CURRENT FILING DATE: 2000-06-08
; PRIOR APPLICATION data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 28
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-287B-28

Query Match      17.8% Score 231.5; DB 4; Length 219;
Best Local Similarity 29.8%; Pred. No. 4.7e-17;
Matches 70; Conservative 35; Mismatches 71; Indels 59; Gaps 8;

DB 52 QTELOSRLREVSRLOQ-----TGG-----PSQNGEGYPMQSL 83
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 7 QGDLASLRALQ-----LQGHNAEKLPARABAPKAGLEAPAVTAGLKIEPPAPGEGNSQS 62
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 84 PEQSSDALEAMENGERSKRAVLTOKOKHSHVLHVPINAT--SKDSDVTEVMQPAL 142
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 63 -----SNKRAIQGAETVLIQDCLQIADSETPTIQKSYTFVFWMLLSF 106
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 143 RRGRLAQGYVRIDAGVLLYSQVLFQDVTFTMGVVSRE-----GQGRQETLFR 196
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 107 KRGSALKEKENKILVKEGYFTYQVLTDTKTAMGHILQKKVHVFGDELSTLTLFR 166
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 197 IRSMPSHPDRAVNSCYAGVFHLHQGDILSVIIPRABAKNLSPHGTFLGFVKL 250
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 167 IONMBETLPN---NSCYAGIAKLEEGDELQALIPRENAQISLSDGDVTFPGALKL 218
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 12
US-09-589-287B-30
; Sequence 30, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokine-alpha
; FILE REFERENCE: PF343P3CI
```

```

; CURRENT APPLICATION NUMBER: US/09/589,287B
; CURRENT FILING DATE: 2000-06-08
; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 30
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-287B-30

Query Match      17.4% Score 227.5; DB 4; Length 219;
Best Local Similarity 28.7%; Pred. No. 1.3e-16;
Matches 64; Conservative 46; Mismatches 78; Indels 35; Gaps 7;

OY 52 QTELOSRLREVSRLOQTGSPQNGEGYPMQSLPEQS-----SDALEAME----- 95
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 7 QGDLASLRALQ-----SHNAEKLPARABAPKAGLEAPAVTAGLKIEPPAPGEGN 58
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 96 NGRSRKRAVLTOKOKHSHVLHVPINAT--SKDSDVTEVMQPALRRGRGLAQGYG 154
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 59 SSQSSRNKRAIQGAETVLIQDCLQIADSETPTIQKSYTFVFWMLLSFKGSALKEKENK 118
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 155 VRIDAGVLLYSQVLFQDVTFTMGVVSRE-----GQGRQETLFRICRSMPSHPDRA 207
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 119 ILVKEGYFTYQVLTDTKTAMGHILQKKVHVFGDELSTLTLFRICIONMBETLPN-- 176
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 208 YNSCYAGVFHLHQGDILSVIIPRABAKNLSPHGTFLGFVKL 250
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 177 -NSCYAGIAKLEEGDELQALIPRENAQISLSDGDVTFPGALKL 218
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 13
US-09-589-287B-38
; Sequence 38, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokine-alpha
; FILE REFERENCE: PF343P3CI
; CURRENT APPLICATION NUMBER: US/09/589,287B
; CURRENT FILING DATE: 2000-06-08
; PRIOR APPLICATION data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 38
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-589-287B-38

Query Match      16.1% Score 210.5; DB 4; Length 289;
Best Local Similarity 28.0%; Pred. No. 1.3e-14;
Matches 76; Conservative 45; Mismatches 109; Indels 41; Gaps 10;
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```

OY 9 LAPGPPGNGMGPVREPAALSVLWLSGALGAACAMA---LITQTELOSRLREVSR 65
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 30 ITPQKEGAWFGICRDRGLAATLL--ALLSSFTMSLYQLAALQADLNLMLTMELOS 87
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 66 QGTGSPQNGEGYPMQSLPEQS-----SDALEAMENGERSRKRAVLTOKOKHSHVL 118
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 88 RGSATPRAAG-----APELTAGVLLTPAARPHNSRGRNRRAFGQPEETQDQVDL 140
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 119 HLVP-----INATSKDSD-----VTEVMQPALRRGRGLAQGYVRIDAGVLLY 166
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 141 SAPAPCPGGRHSQHDNGKNLNIITQDCLQIADSDTPALEKEKNKIVRQTYGFTY 200
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 167 SQVLFQDVTFTMGVVSRE-----GQGRQETLFRICRSMPSHPDRAVNSCYAGVFHL 219
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 201 SQVLTDTPTIFAMGHVILQKKVHVFGDELSTLTLFRICIONMBETLPN---NSCYAGIA 257
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 220 HQGDILSVIIPRABAKNLSPHGTFLGFVKL 250
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
```

Db 258 EEGDEIQLAIPRENAQISRNDDTFFGALKL 288

RESULT 14

US-09-286-529-21
; Sequence 21, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapien
09-286-529-21

Query Match

16.1%; Score 210; DB 4; Length 145;
Best Local Similarity 37.1%; Pred. No. 5.4e-15;
Matches 46; Conservative 27; Mismatches 41; Indels 10; Gaps 3;

Oy 134 TEVMNOPALRRGRGLQAGVGVRIODAGVLYLSQVLFQDVTFTMGQVVSRE-----GQ 187

Db 24 TVPFWLLSRKGNALBEKENKLVKETGFFIYGOVLYTDKTYAMGHILQRKKVHVFGE 83

Oy 188 GROETLFRICIRSMPSHPDRAVNSCYSGAVFHLHOGDILSVIIPRAKALNLSPHGTFLG 246

Db 84 LSLVTLFRICIQWNPETLPN---NSCYSAGIAKLEGEDELQLAIPRENAQISLDDGVTFEG 140

Oy 247 FVKL 250

Db 141 ALKL 144

RESULT 15

US-09-589-287B-23
; Sequence 23, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF34393C1
; CURRENT APPLICATION NUMBER: US/09/589,287B
; CURRENT FILING DATE: 2000-06-08
; Prior application data removed - check PAM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-287B-23

Query Match

16.0%; Score 208; DB 4; Length 155;
Best Local Similarity 37.1%; Pred. No. 9.8e-15;
Matches 46; Conservative 26; Mismatches 42; Indels 10; Gaps 3;

Oy 134 TEVMNOPALRRGRGLQAGVGVRIODAGVLYLSQVLFQDVTFTMGQVVSRE-----GQ 187

Db 34 TVPFWLLSRKGNALBEKENKLVKETGFFIYGOVLYTDPIFAMGHVIOKKVHVFGE 93

Oy 188 GROETLFRICIRSMPSHPDRAVNSCYSGAVFHLHOGDILSVIIPRAKALNLSPHGTFLG 246

Db 94 LSLVTLFRICIQWNPETLPN---NSCYSAGIAKLEGEDELQLAIPRENAQISRNDDTFFG 150

Oy 247 FVKL 250

Db 151 ALKL 154

Search completed: March 26, 2003, 07:34:21
Job time : 16 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 07:34:09 ; Search time 36 Seconds
(without alignments)
925.352 Million cell updates/sec

Title: US-09-724-341-8

Perfect score: 250
Sequence: 1 MPASSPFLAPKGPQGNMG.....RARKLNTSPHGTFLGFLVKL 250

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

rd size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

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14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
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23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	250	100.0	250	20	AAV06485 Human tumour-a880C
2	250	100.0	250	20	AAV17832 Human PRO715 prote
3	250	100.0	250	20	AAV04283 Human APRIL protei
4	250	100.0	250	20	AAW88368 Tumour necrosis fa
5	250	100.0	250	21	AAV93692 Amino acid sequenc
6	250	100.0	250	21	AA801323 Human PRO715 polyp
7	250	100.0	250	22	AA809243 Human APRIL protei
8	250	100.0	250	22	AA852329 Human TRDL-1alpha
9	250	100.0	250	22	AAV1981 Human TNF and Apol
10	250	100.0	250	23	AAU99305 Human tumour necro

11	250	100.0	250	23	AB881486 Human ZTNF2 amino
12	250	100.0	250	23	ABP47228 Human Blys binding
13	250	100.0	250	23	AAU79155 Human APRIL (a pro
14	246	98.4	247	20	AAV28836 Human TNF-related
15	246	98.4	247	22	AA862327 Human TRDL-1gamma
16	202	80.8	205	20	AAV22225 Human TNF12 protei
17	183	73.2	233	23	AAU99508 Human tumour necro
18	183	73.2	233	23	AAU75402 Tumour necrosis fa
19	183	73.2	250	20	AAV05745 Tumour necrosis fa
20	183	73.2	250	23	AAU99510 Human tumour necro
21	183	73.2	250	23	AAU75406 Tumour necrosis fa
22	154	61.6	233	20	AAU09551 Human TRAILK-3 pr
23	154	61.6	230	20	AAW93588 Human TNRL1-beta p
24	154	61.6	250	21	AAV79670 Human death recept
25	154	61.6	250	23	AAE15502 Human APRIL G70 pr
26	154	61.6	260	20	AAV60542 Human normal bladd
27	154	61.6	260	21	AA854342 Human pancreatic c
28	152	60.8	248	23	AAE15482 Human APRIL G70 pr
29	147	58.8	147	20	AAW88369 Tumour necrosis fa
30	146	58.4	172	22	AAE05055 Protein of a FLAG
31	142	56.8	172	22	AAE05055 Human tumour necro
32	142	56.8	233	18	AAW37002 A fragment of huma
33	136	54.4	136	21	AA808661 Human APRIL (a pro
34	136	54.4	136	23	AAU79142 Human APRIL protei
35	130	52.0	248	22	AAE07877 Gene 44 human secr
36	130	49.2	123	22	AA864873 Human tumour necro
37	121	48.4	168	18	AAW37003 Human tumour necro
38	121	48.4	168	23	AAU99509 Tumour necrosis fa
39	121	48.4	168	23	AAU75403 Human TNF-related
40	121	48.4	234	20	AAV28835 Human TRDL-1beta p
41	121	48.4	234	22	AA862330 Human tumour necro
42	121	48.4	234	23	AAU99511 Tumour necrosis fa
43	121	48.4	234	23	AAU75407 Human prostate tum
44	121	48.4	244	20	AAV74026 Mouse FLAG-tagged
45	121	48.4	149	23	AAE15499 Protein of a FLAG-
46	121	48.4	149	23	AAE15437 Human-mouse APRIL
47	121	48.4	199	23	AAE15503 Mouse APRIL protei
48	121	48.4	232	20	AAV79672 Mouse death recept
49	121	48.4	232	21	AAV79672 Mouse APRIL protei
50	121	48.4	232	22	AAE07878 Murine myc tagged
51	121	48.4	234	22	AAE05054 Mouse APRIL/G70 pr
52	121	48.4	240	23	AAE15483 Mouse TNRL1-beta p
53	121	48.4	241	20	AAV93589 Protein of a myc-t
54	121	48.4	249	23	AAO14131 Human TRDL-1gamma
55	14	3.2	15	22	AA862328 Arabidopsis thalia
56	8	3.2	184	21	AA807407 Arabidopsis thalia
57	8	3.2	223	21	AA807406 Arabidopsis thalia
58	7	2.8	20	23	AAU90178 Insulin/insulin-11
59	7	2.8	20	23	AAU90722 Insulin/insulin-11
60	7	2.8	27	21	AA818725 Amino acid sequenc
61	7	2.8	31	21	AA818726 Amino acid sequenc
62	7	2.8	31	21	AA812436 Dermaseptin B amin
63	7	2.8	32	21	AA818748 A mature dermasept
64	7	2.8	45	19	AAW34538 Lipase signal pepc
65	7	2.8	61	22	AAW86507 Human immune/haema
66	7	2.8	62	21	AA816374 Eucalyptus grandis
67	7	2.8	65	22	ABG12805 Novel human diagno
68	7	2.8	73	22	AAW84103 Human immune/haema
69	7	2.8	78	21	AA818724 A dermaseptin prec
70	7	2.8	79	22	AA864816 Human secreted pro
71	7	2.8	83	22	AAW89786 Human immune/haema
72	7	2.8	87	22	AAU44493 Propionibacterium
73	7	2.8	96	20	AAW82267 Human NTN-2 protei
74	7	2.8	96	20	AAW82269 Human NTN-2 partia
75	7	2.8	105	22	AAW08376 Human polypeptide
76	7	2.8	117	22	AA864874 Human secreted pro
77	7	2.8	133	23	AAU79152 Rat Neutrokin-1alp
78	7	2.8	141	21	AAU71040 Streptococcus pyog
79	7	2.8	142	21	AA808258 Consensus E/F regi
80	7	2.8	142	21	AA858966 Arabidopsis thalia
81	7	2.8	142	23	AAU10946 AGP-3 consensus E/
82	7	2.8	144	21	AA808270 Amino acid sequenc
83	7	2.8	144	21	AAV97038 Soluble murine TNF

84	7	2.8	147	21	AAB08271	Amino acid sequenc
85	7	2.8	147	22	ABBI2145	Human liver cell p
86	7	2.8	150	19	AAM62463	Mouse T cell surfa
87	7	2.8	152	23	AAU79149	Rat Neutrokine- α p
88	7	2.8	153	21	AAV97036	Soluble human TNF
89	7	2.8	153	21	AAAI0136	Arabidopsis thalia
90	7	2.8	155	21	AAB08714	A murine neutrokin
91	7	2.8	155	21	AAV71044	Streptococcus pyog
92	7	2.8	155	23	AAU79143	Mouse Neutrokine-a
93	7	2.8	158	19	AAM81328	TNF2-3, a TNF- α p
94	7	2.8	158	22	ABB76582	Human TNF α 3. Homo
95	7	2.8	158	23	ABB07276	Human TNF- α an
96	7	2.8	159	21	AAV71041	Streptococcus pyog
97	7	2.8	163	21	AAAG21362	Zea mays protein f
98	7	2.8	165	23	AAU79150	Rat Neutrokine- α p
99	7	2.8	167	21	AAV71046	Streptococcus pyog
100	7	2.8	177	21	AAB08664	A murine neutrokin

ALIGNMENTS

RESULT 1

AAV06485 standard; Protein; 250 AA.

ID AAY06485;

AC AAY06485;

XX 27-SEP-1999 (first entry)

XX Human tumour-associated protein PRO715.

XX PRO715; UNQ383; cancer; tumour necrosis family; diagnosis; therapy;

XX human.

XX Homo sapiens.

XX MO9935170-A2.

XX 15-JUL-1999.

XX 05-JAN-1999; 99WO-US00106.

XX 20-NOV-1998; 98US-0109304.

XX 05-JAN-1998; 98US-0070440.

XX 29-APR-1998; 98US-0083500.

XX 22-MAY-1998; 98US-0086414.

XX 10-JUN-1998; 98US-0088742.

XX 10-NOV-1998; 98US-0107783.

XX (GETH) GENENTECH INC.

XX Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA;

XX Roy MA, Wood WI;

XX WPI; 1999-430385/36.

XX N-PSDB; AAX87262.

XX Antibody against proteins expressed in neoplastic cells, useful for

XX tumor diagnosis and treatment

XX Example 1; Fig 18; 162pp; English.

XX This sequence represents human PRO715 (UNQ382), a protein encoded

XX by the novel cDNA clone DNA52722 (see AAX87262) that shows homology

XX to members of the tumour necrosis factor family. Amplification of

XX DNA52722 was observed in various colon and lung tumors and cell

XX lines, suggesting a role in tumour formation or growth. Antagonists

XX (e.g. antibodies) directed to PRO715 may have use in cancer therapy.

XX The invention identifies 14 genes (see AAX87254-67) that are amplified

XX in the genome of tumour cells. Such amplification is expected to be

XX associated with overexpression of the gene product and to contribute

XX to tumorigenesis. The encoded proteins (see AAY06477-90) may be

CC useful targets for the diagnosis and/or treatment (including
CC prevention) of certain cancers, and may act as predictors of the
CC prognosis of tumour treatment. Antibodies that bind the proteins
CC are claimed and used in claimed cancer diagnostic kits.

SQ Sequence 250 AA;

Query Match 100.0%; Score 250; DB 20; Length 250;
Best Local Similarity 100.0%; Pred. No. 2e-234;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1

Db 1

Oy 61

Db 61

Oy 121

Db 121

Oy 181

Db 181

Oy 241

Db 241

Oy 241

Db 241

Oy 241

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XX DR WP1; 1999-371118/31.
 XX DR N-PSDB; AAX80057.
 XX PT Nucleic acids encoding PRO secreted and transmembrane proteins
 XX PS Claim 12; Fig 31; 123pp; English.
 CC The present invention describes nucleic acids encoding PRO secreted and
 CC transmembrane proteins used therapeutically. The PRO proteins have
 CC cytosolic, anti-inflammatory, anti-proliferative and immunosuppressive
 CC activity. The proteins and polynucleotides can be used in therapy,
 CC identification of homologues, raising antibodies and design of probes
 CC and primers. They can be used in a range of diseases related to proteins
 CC that they have homology with, e.g. a PRO protein having homology to
 CC complement proteins may be used in inflammatory responses.
 XX CC
 SQ Sequence 250 AA;
 Query Match 100.0%; Score 250; DB 20; Length 250;
 Best Local Similarity 100.0%; Pred. No. 2e-234;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPASSPFLAKKPPGNGGVPREPALSVLWLSWGAALGAVACAMALLTQOTELQSLRR 60
 DB 1 MPASSPFLAKKPPGNGGVPREPALSVLWLSWGAALGAVACAMALLTQOTELQSLRR 60
 QY 61 EVSRLOGTGSPSONGEGYPMQSLPEQSSDLEAMNGERSRKRRAVLTOKOKOHSLVHL 120
 DB 61 EVSRLOGTGSPSONGEGYPMQSLPEQSSDLEAMNGERSRKRRAVLTOKOKOHSLVHL 120
 QY 121 VPINATSKDDSDYTEVWMPALRRGRGLQAGYGVRIQDAGVLLYSQVLFQDVTFTMGQ 180
 DB 121 VPINATSKDDSDYTEVWMPALRRGRGLQAGYGVRIQDAGVLLYSQVLFQDVTFTMGQ 180
 QY 181 VVSREGGQROETLFRCTIRSMSPSHDRAVNSCYAGVFHLLHQGDILSVIIPRAKLNLS 240
 DB 181 VVSREGGQROETLFRCTIRSMSPSHDRAVNSCYAGVFHLLHQGDILSVIIPRAKLNLS 240
 QY 241 HGTFLGFVKL 250
 DB 241 HGTFLGFVKL 250
 RESULT 3
 AAY04283
 ID AAY04283 standard; Protein: 250 AA.
 AAY04283;
 DT 17-JUN-1999 (first entry)
 XX DE Human APRIL protein sequence.
 XX KW APRIL; tumour necrosis factor; TNF; proliferating inducing agent;
 KM immune disorder; cancer.
 XX OS Homo sapiens.
 XX PN WO9912965-A2.
 XX PD 18-MAR-1999.
 XX PF 11-SEP-1998; 98WO-US19191.
 XX PR 26-MAR-1998; 98US-0079384.
 XX PR 12-SEP-1997; 97US-0058786.
 XX PA (BIOJ) BIOGEN INC.
 XX PI Techopp J;
 XX DR WP1; 1999-215028/18.

XX DR N-PSDB; AAX30124.
 XX PT A Proliferating Inducing Agent (APRIL), a member of the Tumour
 XX PT Necrosis Factor Family - useful as diagnostic agents and for
 XX PT prevention or treatment of immune disorders and cancer
 XX PS Claim 12; Page 46; 47pp; English.
 CC The present sequence represents a proliferating inducing agent (APRIL)
 CC isolated from human. APRIL is a member of the tumour necrosis factor
 CC family, and essentially free of normally associated proteins. APRIL and
 CC APRIL antibodies are useful in pharmaceutical compositions for
 CC preventing or reducing severity of an autoimmune disease or an immune
 CC response to tissue graft. The composition is also useful for stimulating
 CC or suppressing the immune system, and treating cancer. APRIL is also
 CC useful for treating APRIL-related disorders by delivering via a vector
 CC (preferably viral vector) (gene therapy) into a mammalian (preferably
 CC human) cell. Labeled APRIL and fragments are useful for identifying
 CC APRIL receptors by screening compositions. Antisense DNA and antibodies
 CC and modified APRIL (preferably an anti-APRIL receptor antibody) are
 CC useful as blocking agents for inducing cell death by interfering with
 CC APRIL receptors. The blocking agent is preferably administered with
 CC interferon- γ and treats, suppresses or alters an immune response
 CC involving a signalling pathway between APRIL and its receptor
 CC (preferably involving human carcinoma cells); and also treats,
 CC suppresses or alters the progression of cancer (preferably at least one
 CC chemotherapeutic agent is also administered, and radiation therapy is
 CC also given to the patient.
 XX CC
 SQ Sequence 250 AA;
 Query Match 100.0%; Score 250; DB 20; Length 250;
 Best Local Similarity 100.0%; Pred. No. 2e-234;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPASSPFLAKKPPGNGGVPREPALSVLWLSWGAALGAVACAMALLTQOTELQSLRR 60
 DB 1 MPASSPFLAKKPPGNGGVPREPALSVLWLSWGAALGAVACAMALLTQOTELQSLRR 60
 QY 61 EVSRLOGTGSPSONGEGYPMQSLPEQSSDLEAMNGERSRKRRAVLTOKOKOHSLVHL 120
 DB 61 EVSRLOGTGSPSONGEGYPMQSLPEQSSDLEAMNGERSRKRRAVLTOKOKOHSLVHL 120
 QY 121 VPINATSKDDSDYTEVWMPALRRGRGLQAGYGVRIQDAGVLLYSQVLFQDVTFTMGQ 180
 DB 121 VPINATSKDDSDYTEVWMPALRRGRGLQAGYGVRIQDAGVLLYSQVLFQDVTFTMGQ 180
 QY 181 VVSREGGQROETLFRCTIRSMSPSHDRAVNSCYAGVFHLLHQGDILSVIIPRAKLNLS 240
 DB 181 VVSREGGQROETLFRCTIRSMSPSHDRAVNSCYAGVFHLLHQGDILSVIIPRAKLNLS 240
 QY 241 HGTFLGFVKL 250
 DB 241 HGTFLGFVKL 250
 RESULT 4
 AAW88368
 ID AAW88368 standard; Protein: 250 AA.
 AAW88368;
 AC AAW88368;
 DT 26-APR-1999 (first entry)
 XX DE Tumour necrosis factor-gamma.
 XX KW Tumour necrosis factor-gamma; TNF-gamma; human; inflammation;
 KM cancer; tumour; metastasis; graft versus host disease;
 KM drug screening; therapy; diagnosis.
 XX OS Homo sapiens.
 XX PN WO9900518-A1.

XX 07-JAN-1999.
 PD 12-JUN-1998; 98WO-US12101.
 XX 26-JUN-1997; 97US-0883086.
 XX (ABBO) ABBOTT LAB.
 XX Wiley SR;
 PI WPI: 1999-095761/08.
 DR N-PSDB; AAX06771.
 XX Tumour necrosis factor gamma detects target polynucleotides - useful
 PT for, e.g. treating inflammation, cancer and graft versus host
 PT disease
 PT
 XX Claim 16; Page 84-85; 106pp; English.

This is the amino acid sequence of human tumour necrosis factor gamma (TNFG), a novel member of the TNF family of ligands. The invention provides a method of producing TNFG polypeptide using a recombinant expressing system comprising a nucleic acid sequence (see AAX06771) encoding TNFG and transformed host cells. Also provided are a procedure of producing biologically active soluble TNFG (see AAW8369), which can be used to treat deficiencies of TNFG and disease conditions ameliorated by TNFG. Antibodies, CC and agonists and inhibitors of such a polypeptide may be used to treat TNFG-associated diseases, tumours or metastases, and to screen for, diagnose and monitor conditions attributable to TNFG, CC especially inflammation, cancer and graft versus host disease. CC Cells expressing TNFG on their surface can be used to screen for (ant)agonists, and to detect receptor binding.

XX Sequence 250 AA;

Query Match 100.0%; Score 250; DB 20; Length 250;
 Best Local Similarity 100.0%; Pred. No. 2e-234;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MPASSPFLAPKPGPNMGVREPALVALWLSGALGAVACAMALLTQOTELQSLRR 60
 DB 1 MPASSPFLAPKPGPNMGVREPALVALWLSGALGAVACAMALLTQOTELQSLRR 60
 OY 61 EVSRLQGTGSPQNGRGYWGSLPEQSSDALAMWENGERSRRRAVLTQKQKQSHVHL 120
 DB 61 EVSRLQGTGSPQNGRGYWGSLPEQSSDALAMWENGERSRRRAVLTQKQKQSHVHL 120
 OY 121 VPINATSKDSDVTEVMQPALRRGRLQAGYGVRIODAGVYLYSYQLFQDVTFTMQQ 180
 DB 121 VPINATSKDSDVTEVMQPALRRGRLQAGYGVRIODAGVYLYSYQLFQDVTFTMQQ 180
 OY 181 VVSREGQGOETLFRICRSMPSHPDRAVNSYSAVGFHLHQGDILSVIIPRAKINLSP 240
 DB 181 VVSREGQGOETLFRICRSMPSHPDRAVNSYSAVGFHLHQGDILSVIIPRAKINLSP 240
 OY 241 HGTFLGFVKL 250
 DB 241 HGTFLGFVKL 250

RESULT 5
 AAY93692
 ID AAY93692 standard; Protein; 250 AA.
 AC AAY93692;
 XX 03-OCT-2000 (first entry)
 DT
 XX 'Amino acid sequence of novel polypeptide PRO715.
 DE
 XX PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357;

KW PRO715; PRO1017, PRO112, PRO509; PRO853; PRO882; tumour cell;
 KM tumourigenesis; cancer; neoplastic cell growth; cell proliferation.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..40
 FT /note= "signal sequence"
 FT Region 34..45
 FT /note= "prokaryotic membrane lipoprotein attachment site"
 FT Modified-site 36..42
 FT /note= "N-myristoylation site"
 FT Modified-site 40..46
 FT /note= "N-myristoylation site"
 FT Modified-site 124..128
 FT /note= "N-glycosylation site"
 FT Modified-site 156..164
 FT /note= "tyrosine kinase phosphorylation site"
 FT Modified-site 179..185
 FT /note= "N-myristoylation site"
 FT Modified-site 242..248
 FT /note= "N-myristoylation site"

XX WO200037640-A2.
 XX 29-JUN-2000.
 XX 16-DEC-1999; 99WO-US30095.
 XX 22-DEC-1998; 98US-0113286.
 XX 08-MAR-1999; 99WO-US05028.
 XX 02-JUN-1999; 99WO-US12252.
 XX 01-SEP-1999; 99WO-US20111.
 XX 15-SEP-1999; 99WO-US21090.
 XX 30-NOV-1999; 99WO-US28313.
 XX 30-NOV-1999; 99WO-US28409.
 XX 01-DEC-1999; 99WO-US28301.
 XX 02-DEC-1999; 99WO-US28565.

XX (GETH) GENENTECH INC.
 XX Botstein D, Goddard A, Gurney AL, Hillan K, Lawrence DA, Roy MA;
 PI Wood WI;
 XX WPI: 2000-452188/39.
 DR N-PSDB; AAA46928.
 OY New anti-polypeptide antibody useful in the treatment and diagnosis of
 PT neoplastic cell growth and proliferation -
 PT
 OY Claim 61; Fig 18; 220pp; English.

CC The present sequence represents a novel human polypeptide. The
 CC specification describes novel polypeptides designated PRO201, PRO292,
 CC PRO327, PRO1265, PRO344, PRO347, PRO357, PRO1017,
 CC PRO1112, PRO509, PRO853 and PRO882. These genes are amplified in
 CC the genome of tumour cells. The polypeptides are believed to contribute
 CC to tumourigenesis. The polypeptides are useful target for the
 CC identification of certain cancers, and may act as predictors of the
 CC prognosis of tumour treatment. Antibodies against these polypeptides
 CC are useful in the treatment and diagnosis of neoplastic cell growth
 CC and proliferation in mammals.

XX Sequence 250 AA;
 OY Query Match 100.0%; Score 250; DB 21; Length 250;
 Best Local Similarity 100.0%; Pred. No. 2e-234;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MPASSPFLAPKPGPNMGVREPALVALWLSGALGAVACAMALLTQOTELQSLRR 60
 DB 1 MPASSPFLAPKPGPNMGVREPALVALWLSGALGAVACAMALLTQOTELQSLRR 60

QY 61 EVSRLQGTGSPSONGEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTOKOKHOSVHL 120
 DB 61 EVSRLQGTGSPSONGEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTOKOKHOSVHL 120
 QY 121 VPINATSKDSDVTEVWMPALRRGRGLQAGYGVRIODAGVLLYSQVLFQDVTFTMGQ 180
 DB 121 VPINATSKDSDVTEVWMPALRRGRGLQAGYGVRIODAGVLLYSQVLFQDVTFTMGQ 180
 QY 181 VSRREGQROETLFRCTIRSMPSHPDRAYNSCYAGVFHLHOGDILSVIIPRAKAKNLSP 240
 DB 181 VSRREGQROETLFRCTIRSMPSHPDRAYNSCYAGVFHLHOGDILSVIIPRAKAKNLSP 240
 QY 241 HGTFLGFVKL 250
 DB 241 HGTFLGFVKL 250

RESULT 6
 AAB01323 standard; Protein; 250 AA.
 AAB01323;
 AAB01323;
 DT 25-SEP-2000 (first entry)
 XX Human PRO715 polypeptide.
 DE Human PRO715 polypeptide.
 XX PRO; membrane bound protein; secreted proteain; PRO357; PRO327;
 KW PRO243; PRO715; PRO341; PRO323; PRO399; PRO344; PRO347;
 KW PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide;
 KW antibody; screening; detection; inhibition; probe; primer; human.
 XX Homo sapiens.
 OS Homo sapiens.
 XX Key location/Qualifiers
 FH Peptide 1..40
 FT /label= Signal peptide
 FT Domain 34..45
 FT /label= Prokaryotic membrane lipoprotein lipid attachment site

FT Modified-site 36..42 "N-myristoylation site"
 FT /note= 40..46
 FT Modified-site /note= "N-myristoylation site"
 FT Modified-site 124..128
 FT /note= "N-glycosylation site"
 FT Modified-site 156..164
 FT /note= "Tyrosine kinase phosphorylation site"
 FT Modified-site 179..185
 FT /note= "N-myristoylation site"
 FT Modified-site 242..248
 FT /note= "N-myristoylation site"

PT Modified-site
 PN WO200032776-A2.
 XX 08-JUN-2000.
 PD 01-DEC-1999; 99WO-US28301.
 XX 01-DEC-1998; 98WO-US25108.
 PR 16-DEC-1998; 98US-0112850.
 PR 22-DEC-1998; 98US-0113296.
 XX (GETH) GENENTECH INC.
 PA Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E,
 PI Gerltsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL,
 PI Hillan KJ, Kijavini J, Napier MA, Roy MA, Tumas D, Wood WJ;
 XX WPI; 2000-41324/35.
 DR N-PSDB; AAA49565.
 XX New human nucleic acids encoding secreted and transmembrane

PT polypeptides, designated as PRO polypeptides, useful as pharmaceutical
 PT and diagnostic agents
 XX Claim 12, Fig 28; 187pp; English.

CC New human nucleic acids encoding secreted and transmembrane
 CC polypeptides which are designated as PRO polypeptides are described
 CC The membrane-bound proteins have various industrial applications,
 CC including as pharmaceutical and diagnostic agents. The membrane-bound
 CC proteins can also be employed for screening of potential peptide or
 CC small molecule inhibitors of the relevant receptor/ligand interaction.
 CC Anti-PRO antibodies are useful for the affinity purification of PRO
 CC from recombinant cell culture or natural sources.
 XX Sequence 250 AA;

Query Match 100.0%; Score 250; DB 21; Length 250;
 Best Local Similarity 100.0%; Pred. No. 2e-234;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPASSPFLAPKGPFGNMGSPVREPALSVLMTLSMGALGAVACAMALLTQOTELQSLRR 60
 DB 1 MPASSPFLAPKGPFGNMGSPVREPALSVLMTLSMGALGAVACAMALLTQOTELQSLRR 60
 QY 61 EVSRLQGTGSPSONGEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTOKOKHOSVHL 120
 DB 61 EVSRLQGTGSPSONGEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTOKOKHOSVHL 120
 QY 121 VPINATSKDSDVTEVWMPALRRGRGLQAGYGVRIODAGVLLYSQVLFQDVTFTMGQ 180
 DB 121 VPINATSKDSDVTEVWMPALRRGRGLQAGYGVRIODAGVLLYSQVLFQDVTFTMGQ 180
 QY 181 VSRREGQROETLFRCTIRSMPSHPDRAYNSCYAGVFHLHOGDILSVIIPRAKAKNLSP 240
 DB 181 VSRREGQROETLFRCTIRSMPSHPDRAYNSCYAGVFHLHOGDILSVIIPRAKAKNLSP 240
 QY 241 HGTFLGFVKL 250
 DB 241 HGTFLGFVKL 250

RESULT 7
 AAE09243 standard; Protein; 250 AA.
 ID AAE09243
 XX AAE09243;
 AC 19-NOV-2001 (first entry)
 DT Human APRIL protein.
 XX Human APRIL protein.
 XX Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
 KW TNFR; TACI; BCMA; therapy; cancer; leukemia; myeloma; lymphoma;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
 KW psoriasis.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO200160397-A1.
 PN 23-AUG-2001.
 PD 28-NOV-2000; 2000WO-US32378.
 XX 16-FEB-2000; 2000US-0182938.
 PR 22-AUG-2000; 2000US-0226986.
 XX (GETH) GENENTECH INC.
 PA Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM,
 PI Yan WJ;
 XX WPI; 2001-541628/60.

DR N-PSDB; AAD15904.
 XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
 PT activity, for treating autoimmune disorders and cancer, comprises
 FT exposing the cells to TALL-1 or APRIL polypeptide agonists or
 PT antagonists -
 XX
 PS Claim 20; Fig 4; 160pp; English.
 XX
 CC The invention relates to methods of using one or more agonists or
 CC antagonists to modulate the activity of the members of TNF (tumour
 CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)
 CC e.g. TNF1 or BCMA. The method is useful for treating pathological
 CC conditions or diseases associated with increased TALL-1 and APRIL
 CC expression or activity. TALL-1 and APRIL antagonists are used to
 CC block the interaction between APRIL and TALL-1 with TNF1 or BCMA.
 CC They are useful for treating a mammal suffering from cancer such
 CC as leukaemia, lymphoma, myeloma, cancers of lung and colon and
 CC autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,
 CC psoriasis and lupus erythematosus. The present sequence is human
 CC APRIL protein.

SO Sequence 250 AA;
 Query Match 100.0%; Score 250; DB 22; Length 250;
 Best Local Similarity 100.0%; Pred. No. 2e-234;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MPASSPFLAARKPGPNMGVPRREPALSVALMLSMGALGAVACAMALLTQOTELQSLRR 60
 DB 1 MPASSPFLAARKPGPNMGVPRREPALSVALMLSMGALGAVACAMALLTQOTELQSLRR 60
 OY 61 EVSRLQGTGSPQNGEGYPMQSLPEQSSDALEAMENGERSKRRRAVLTKOKKHSHVHL 120
 DB 61 EVSRLQGTGSPQNGEGYPMQSLPEQSSDALEAMENGERSKRRRAVLTKOKKHSHVHL 120
 OY 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYGVRIODAGVLLYSQVLFQDVTFTMGQ 180
 DB 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYGVRIODAGVLLYSQVLFQDVTFTMGQ 180
 OY 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYGVRIODAGVLLYSQVLFQDVTFTMGQ 180
 DB 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYGVRIODAGVLLYSQVLFQDVTFTMGQ 180
 OY 181 VVSREGQGRQETLFRICRSMSPHPDRAVNSCYSAVFHLHOGDILSVIIPRAAKLNLS 240
 DB 181 VVSREGQGRQETLFRICRSMSPHPDRAVNSCYSAVFHLHOGDILSVIIPRAAKLNLS 240
 OY 241 HGTFLGFVKL 250
 DB 241 HGTFLGFVKL 250

RESULT 8
 AAB62329
 ID AAB62329 standard; protein; 250 AA.

AC AAB62329;
 DT 29-JUN-2001 (first entry)
 XX
 DE Human TRDL-1alpha polypeptide.
 XX
 KW Tumour necrosis factor related death ligand-1gamma; TRDL-1gamma; TRDL;
 KW cell death; apoptosis; human; TRDL-1alpha.
 XX
 OS Homo sapiens.
 PN WO200125256-A2.
 PD 12-APR-2001.
 PF 06-OCT-2000; 2000MO-US27868.
 PR 06-OCT-1999; 99US-0157913.
 PA (UTAH) UNIV UTAH RES FOUND.

XX Jones D, Manos E;
 PI
 XX WPI; 2001-261728/29.
 DR
 XX Isolated and purified polynucleotide encoding human tumor necrosis
 PT factor related death ligand (TRDL)-1 gamma useful for identifying
 PT agents that inhibit or enhance TRDL-1 gamma mediated induction of
 PT apoptosis -
 XX
 PS Disclosure; Fig 1; 39pp; English.
 XX
 CC The invention provides a human tumour necrosis factor related death
 CC ligand-1gamma (TRDL-1gamma). The TRDL-1gamma polypeptide can be
 CC expressed by standard recombinant methodology. TRDL-1gamma stimulates
 CC Jurkat cell death. It is useful for identifying agents capable of
 CC inhibiting or enhancing TRDL-1gamma mediated induction of apoptosis.
 CC The present sequence represents a TRDL-1alpha polypeptide, used in
 CC alignment studies.

SO Sequence 250 AA;

Query Match 100.0%; Score 250; DB 22; Length 250;
 Best Local Similarity 100.0%; Pred. No. 2e-234;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MPASSPFLAARKPGPNMGVPRREPALSVALMLSMGALGAVACAMALLTQOTELQSLRR 60
 DB 1 MPASSPFLAARKPGPNMGVPRREPALSVALMLSMGALGAVACAMALLTQOTELQSLRR 60
 OY 61 EVSRLQGTGSPQNGEGYPMQSLPEQSSDALEAMENGERSKRRRAVLTKOKKHSHVHL 120
 DB 61 EVSRLQGTGSPQNGEGYPMQSLPEQSSDALEAMENGERSKRRRAVLTKOKKHSHVHL 120
 OY 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYGVRIODAGVLLYSQVLFQDVTFTMGQ 180
 DB 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYGVRIODAGVLLYSQVLFQDVTFTMGQ 180
 OY 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYGVRIODAGVLLYSQVLFQDVTFTMGQ 180
 DB 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYGVRIODAGVLLYSQVLFQDVTFTMGQ 180
 OY 181 VVSREGQGRQETLFRICRSMSPHPDRAVNSCYSAVFHLHOGDILSVIIPRAAKLNLS 240
 DB 181 VVSREGQGRQETLFRICRSMSPHPDRAVNSCYSAVFHLHOGDILSVIIPRAAKLNLS 240
 OY 241 HGTFLGFVKL 250
 DB 241 HGTFLGFVKL 250

RESULT 9
 AAY71981
 ID AAY71981 standard; protein; 250 AA.

AC AAY71981;
 DT 28-MAR-2001 (first entry)
 XX
 DE Human TNF and Apol-related Leucocyte-expressed ligand 2/APRIL protein.
 XX
 KW Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
 KW Tumour necrosis factor and Apol-related Leucocyte expressed ligand;
 KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
 KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
 KW thrombocytopenia purpura; acute rheumatic fever; myasthenia gravis;
 KW haemolytic anaemia; Grave's disease; Goodpasture's syndrome; TALL2/APRIL;
 KW post-streptococcal glomerulonephritis; polyarthritis nodosa; BCMA;
 KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
 OS
 XX Homo sapiens.
 PF
 FH Key Location/Qualifiers
 FT Domain 28..48
 FT /label= Transmembrane_domain
 FT Region 116..122
 FT /label= Beta_strand

FT Region 138..140
 FT /label= Beta_strand
 FT 148..150
 FT /label= Beta_strand
 FT 153..156
 FT /label= Beta_strand
 FT 162..173
 FT /label= Beta_strand
 FT 187..192
 FT /label= Beta_strand
 FT 201..209
 FT /label= Beta_strand
 FT 210..217
 FT /label= Beta_strand
 FT 222..230
 FT /label= Beta_strand
 FT 243..250
 FT /label= Beta_strand

XX WO200068378-A1.

PD 16-NOV-2000.

XX 05-MAY-2000; 2000WO-US12266.

XX 06-MAY-1999; 99US-0132892.

PR 01-MAY-2000; 2000US-0201012.

XX (NAME-) NAT JEWISH MEDICAL & RES CENT.

XX Shu HS;

DR WPI; 2001-016094/02.

PT Isolated TALL-1 protein is used to identify compounds that regulate B lymphocyte proliferation, used to treat B lymphocyte associated autoimmune disorders -

XX Example 1; Fig 1a; 112pp; English.

CC The present invention relates to Tumour necrosis factor (TNF) and Abp-related leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules, proteins (including homologues), and their antibodies. The invention in particular relates to methods for regulating the interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to regulate monocyte, macrophage and B lymphocyte mediated immune responses. TALL-1 protein is useful for identifying compounds that regulate B lymphocyte proliferation. It is also useful for treating B lymphocyte associated autoimmune disorders like rheumatoid arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes mellitus, multiple sclerosis, myasthenia gravis, Grave's disease, autoimmune hemolytic anaemia, autoimmune thrombocytopenia, purpura, Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, post-streptococcal glomerulonephritis, or polyarteritis nodosa. CC The TALL-1 protein and its corresponding nucleic acid sequence are also useful in diagnostic assays.

CC The present sequence is human Tumour necrosis factor (TNF) and CC Apol-related leucocyte-expressed Ligand 2 (TALL-2)/APRIL protein. CC TALL-2/APRIL is encoded by the second TNF/PaSL like gene. TALL2/APRIL also belongs to the subfamily of TNF family of ligands.

XX Sequence 250 AA;

Query Match 100.0%; Score 250; DB 22; Length 250;

Best Local Similarity 100.0%; Pred. NO. 2e-234; Mismatches 0; Gaps 0;

Matches 250; Conservative 0; Indels 0; Gaps 0;

QY 1 MPASSPFLAPKGPNGMGPVREPALSVALLSWGALGAVACAMALLTOOTELQSLRR 60

DB 1 MPASSPFLAPKGPNGMGPVREPALSVALLSWGALGAVACAMALLTOOTELQSLRR 60

QY 61 EVSRLOGTGCPSONGEGYPMQSLPEQSSDALEAWNGERSRKRRAVLTQOKKQHSVLHL 120

DB 61 EVSRLOGTGCPSONGEGYPMQSLPEQSSDALEAWNGERSRKRRAVLTQOKKQHSVLHL 120

QY 121 VPINATSKDSDVTEVMMQPALRRGRLQAGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180

DB 121 VPINATSKDSDVTEVMMQPALRRGRLQAGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180

QY 181 VSRREGQROETLFRICIRSMPSHPDRAYNSCYSGVFHLHOGDILSVIIPRAAKLNLSP 240

DB 181 VSRREGQROETLFRICIRSMPSHPDRAYNSCYSGVFHLHOGDILSVIIPRAAKLNLSP 240

QY 241 HGTFLGFVKL 250

DB 241 HGTFLGFVKL 250

RESULT 10

AAU99305 standard; Protein; 250 AA.

AC AAU99305;

DT 24-SEP-2002 (first entry)

XX Human tumour necrosis factor ligand (TNFL), TRASH protein #1.

XX Human; anti-inflammatory; immunomodulatory; TRASH; TNFL; TANGO 118;

XX tumour necrosis factor ligand; signal transduction; gene therapy;

XX diagnosis; immune response; inflammatory disorder;

XX differential disorder; developmental disorder.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

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XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

PT New nucleic acid encoding a protein designated TRASH is a member of the PT tumor necrosis factor ligand superfamily of proteins and is useful to PT detect and treat TRASH-associated disorders including immune and PT inflammatory disorders -

XX Claim 28; Fig 1; 44pp; English.

XX The invention discloses an isolated nucleic acid encoding a novel tumour CC necrosis factor ligand (TNFL), referred to as TRASH (not defined) (or CC TANGO 118), protein. Members of the TNFL superfamily are involved in the CC activation of a large array of cellular genes and of multiple signal

transduction pathways, kinases and transcription factors. The nucleic acid and protein can be used in gene therapy, to identify compounds that modulate TRASH activity, raise antibodies and treat, or diagnose, disorders associated with aberrant TRASH activity or expression, particularly an immune response or inflammatory disorder, or a differentiative or developmental disorder. The sequence presented is the human tumour necrosis factor ligand (TNFL), TRASH protein #1.

SQ Sequence 250 AA;

Query Match 100.0%; Score 250; DB 23; Length 250;

Best Local Similarity 100.0%; Pred. No. 2e-234; Mismatches 0; Indels 0; Gaps 0;

Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPASSPFLAPKGPNGMGVREPALSVLWLSGALGAVACAMALLTQOTELQSLRR 60
DB 1 MPASSPFLAPKGPNGMGVREPALSVLWLSGALGAVACAMALLTQOTELQSLRR 60
QY 61 EVSRLQGTGSPQNGEGYPMQSLPEQSSDALAWENGERSRRRAVLTQKKQHSVHL 120
DB 61 EVSRLQGTGSPQNGEGYPMQSLPEQSSDALAWENGERSRRRAVLTQKKQHSVHL 120
QY 121 VPINATSKDDSDVTEVMQPALRKGGLQAGYGVRIODAGVYLVSQVLPDQVFTMGQ 180
DB 121 VPINATSKDDSDVTEVMQPALRKGGLQAGYGVRIODAGVYLVSQVLPDQVFTMGQ 180
QY 181 VVSREGQROETLFCIRSMSPHPDRAVNSCYAGVFHLHOGDILSVIIPARAKLNLSP 240
DB 181 VVSREGQROETLFCIRSMSPHPDRAVNSCYAGVFHLHOGDILSVIIPARAKLNLSP 240
QY 241 HGTFLGFVKL 250
DB 241 HGTFLGFVKL 250

RESULT 11

ABP47228 ID ABP47228 standard; Protein; 250 AA.

AC ABP47228;

DT 02-SEP-2002 (first entry)

DE Human ZTNF2 amino acid sequence SEQ ID NO:6.

Human: Ztnfr2; tumour necrosis factor receptor; cytostatic; immunosuppressive; dermatological; antiinflammatory; antidiabetic; neuroprotective; antineumatic; antiaesthetic; antiaesthetic; neoplastic; hypotensive; gene therapy; B lymphocyte; tumour; autoimmune disorder; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; insulin dependent diabetes mellitus; asthma; rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma; glomerulonephritis; vasculitis; chronic lymphoid leukemia; nephritis; pyelonephritis; renal neoplasia; multiple myeloma; amyloidosis; light chain neuropathy; hypertension; large vessel disease; graft-versus host disease; graft rejection; Crohn's disease.

Homo sapiens.

WO200238766-A2.

PD 16-MAY-2002.

PF 05-NOV-2001; 2001WO-US47018.

PR 07-NOV-2000; 2000US-246449P.

PR 20-DEC-2000; 2000US-257131P.

PR 28-JUN-2001; 2001US-301715P.

PR 29-AUG-2001; 2001US-315565P.

PA (ZYMO) ZYMOGENETICS INC.

PI Gross JA, Xu W, Henne RM, Grant FU;

XX WPI; 2002-508212/54.

PT Novel isolated human tumour necrosis factor receptor polypeptide, termed Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage renal failure or renal disease and lymphoma

PS Disclosure; Page 135; 154pp; English.

XX The present invention describes a human tumour necrosis factor receptor designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive, dermatological, antiinflammatory, neuroprotective, antidiabetic, antineumatic, antiaesthetic, neoplastic and hypotensive activities, and can be used in gene therapy. (I) can be used for inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12 (e.g. ZTNF4), for treating disorders and diseases associated with B lymphocytes, activated B lymphocytes or resting B lymphocytes, and for inhibiting the proliferation of tumour cells. (I) is useful for treating autoimmune disorders such as systemic lupus erythematosus, myasthenia gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma, rheumatoid arthritis, bronchitis, emphysema and end stage renal failure or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid leukaemia, nephritis, and pyelonephritis, and for treating renal neoplasia, multiple myeloma, lymphomas, light chain neuropathy, or amyloidosis, hypertension, large vessel diseases, graft-versus host disease, graft rejection and Crohn's disease. (I) is useful for modulating the immune system, for regulating B cell responses and development, for modulating development of other cells, antibody production and cytokine production, and for modulating T and B cell communication. The present sequence represents the human ZTNF2 protein which is given in the exemplification of the present invention.

SQ Sequence 250 AA;

Query Match 100.0%; Score 250; DB 23; Length 250;

Best Local Similarity 100.0%; Pred. No. 2e-234; Mismatches 0; Indels 0; Gaps 0;

Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPASSPFLAPKGPNGMGVREPALSVLWLSGALGAVACAMALLTQOTELQSLRR 60
DB 1 MPASSPFLAPKGPNGMGVREPALSVLWLSGALGAVACAMALLTQOTELQSLRR 60
QY 61 EVSRLQGTGSPQNGEGYPMQSLPEQSSDALAWENGERSRRRAVLTQKKQHSVHL 120
DB 61 EVSRLQGTGSPQNGEGYPMQSLPEQSSDALAWENGERSRRRAVLTQKKQHSVHL 120
QY 121 VPINATSKDDSDVTEVMQPALRKGGLQAGYGVRIODAGVYLVSQVLPDQVFTMGQ 180
DB 121 VPINATSKDDSDVTEVMQPALRKGGLQAGYGVRIODAGVYLVSQVLPDQVFTMGQ 180
QY 181 VVSREGQROETLFCIRSMSPHPDRAVNSCYAGVFHLHOGDILSVIIPARAKLNLSP 240
DB 181 VVSREGQROETLFCIRSMSPHPDRAVNSCYAGVFHLHOGDILSVIIPARAKLNLSP 240
QY 241 HGTFLGFVKL 250
DB 241 HGTFLGFVKL 250

RESULT 12

ABP47228 ID ABP47228 standard; Protein; 250 AA.

AC ABP47228;

DT 19-AUG-2002 (first entry)

DE Human Bly's binding scfv VH CDR3 SEQ ID 3239.

XX Bly's; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antineumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US19110.
 XX
 PR 16-JUN-2000; 2000US-212210P.
 PR 17-OCT-2000; 2000US-240816P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 21-MAR-2001; 2001US-277379P.
 PR 25-MAY-2001; 2001US-293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 DR Ruben SM, Baraash SC, Choi GH, Vaughan T, Hilbert D;
 WPI; 2002-114799/15.
 XX
 PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for
 XX the diagnosis and treatment of cancers and immune disorders -
 XX
 PS Disclosure; Page 3147-3148; 3148pp; English.
 XX
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cyostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antineoplastic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method
 CC of the invention.
 XX
 XX Sequence 250 AA;
 Query Match 100.0%; Score 250; DB 23; Length 250;
 Best Local Similarity 100.0%; Pred. No. 2e-234;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPASSPFLAPKGPNGGVPREPALSVALLWSGALGAVACAMALLTQOTELQSLRR 60
 DB 1 MPASSPFLAPKGPNGGVPREPALSVALLWSGALGAVACAMALLTQOTELQSLRR 60
 QY 61 EVSRIOGSGSONEGYPMQSLPEOSSDALAEWNGERSRRRAVLTQKKQKQSVLHL 120
 DB 61 EVSRIOGSGSONEGYPMQSLPEOSSDALAEWNGERSRRRAVLTQKKQKQSVLHL 120
 QY 121 VPINATSKDSDVTEVMWQPALRRGRGLQAOQYGVRIODAGVYLLYSQVLTPODVTFTMGQ 180
 DB 121 VPINATSKDSDVTEVMWQPALRRGRGLQAOQYGVRIODAGVYLLYSQVLTPODVTFTMGQ 180
 QY 181 VVSREGGROETLFFRCIRSPSHPDRAVNSCSAGVFLHOGDILSVIIPARAKLNLSP 240
 DB 181 VVSREGGROETLFFRCIRSPSHPDRAVNSCSAGVFLHOGDILSVIIPARAKLNLSP 240
 QY 241 HGTFLGFVKL 250
 DB 241 HGTFLGFVKL 250

RESULT 13
 AAU79155
 ID AAU79155 standard; Protein; 250 AA.
 XX
 AC AAU79155;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Human APRIL (a proliferation-inducing ligand) protein #2.
 KW Human; Neutroline-alpha; antibody; immunogen; B-cell cancer;
 KW autoimmune disease; Sjogren's syndrome; systemic lupus erythematosus;
 KW rheumatoid arthritis; chronic lymphocytic leukaemia; multiple myeloma;
 KW Hodgkin's lymphoma; non-Hodgkin's lymphoma; hypergammaglobulinemia;
 KW APRIL, a proliferation-inducing ligand.
 XX
 OS Homo sapiens.
 XX
 PN WO200218620-A2.
 XX
 PD 07-MAR-2002.
 XX
 PF 15-AUG-2001; 2001WO-US25549.
 XX
 PR 15-AUG-2000; 2000US-225628P.
 PR 23-AUG-2000; 2000US-227008P.
 PR 22-SEP-2000; 2000US-234338P.
 PR 17-OCT-2000; 2000US-240806P.
 PR 30-NOV-2000; 2000US-250020P.
 PR 06-MAR-2001; 2001US-276248P.
 PR 25-MAY-2001; 2001US-293499P.
 PR 07-JUN-2001; 2001US-296122P.
 PR 13-JUL-2001; 2001US-304809P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA Yu G, Ebner R, Ni J, Rosen CA, Ullrich S;
 WPI; 2002-304259/34.
 XX
 PT An isolated antibody or portion that specifically binds to a protein
 PT useful in the treatment of diseases such as hypergammaglobulinemia and
 PT cancer -
 XX
 PS Claim 1; Page 481-482; 482pp; English.
 XX
 CC The present invention relates to a new antibody, or portion, that
 CC specifically binds to a protein which has a 285 or 250 amino acid
 CC sequence as fully defined in the specification. The antibody of the
 CC invention is useful in treating a disease or disorder such as cancer,
 CC especially B-cell cancer, autoimmune diseases such as Sjogren's
 CC syndrome, systemic lupus erythematosus, rheumatoid arthritis, chronic
 CC lymphocytic leukaemia, multiple myeloma, Hodgkin's lymphoma,
 CC non-Hodgkin's lymphoma or hypergammaglobulinemia, or in diagnosing a
 CC disease or disorder comprising assaying expression of Neutroline-alpha
 CC and APRIL (a proliferation-inducing ligand) in cells or body fluids using
 CC antibodies and comparing the Neutroline-alpha and APRIL expression level
 CC with a standard Neutroline-alpha and APRIL expression level, whereby an
 CC increase or decrease in the assayed Neutroline-alpha and APRIL expression
 CC level compared to the standard levels is indicative of a disease or
 CC disorder. The present amino acid sequence represents the human APRIL
 CC protein #2 of the invention.
 XX
 SQ Sequence 250 AA;
 Query Match 100.0%; Score 250; DB 23; Length 250;
 Best Local Similarity 100.0%; Pred. No. 2e-234;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPASSPFLAPKGPNGGVPREPALSVALLWSGALGAVACAMALLTQOTELQSLRR 60
 DB 1 MPASSPFLAPKGPNGGVPREPALSVALLWSGALGAVACAMALLTQOTELQSLRR 60

OY 61 EVSRLQGTGSPONGEGYPMQSLPEQSSDPALEAENGERSRKRAVLTQKKQKHSVHL 120
 DB 61 EVSRLQGTGSPONGEGYPMQSLPEQSSDPALEAENGERSRKRAVLTQKKQKHSVHL 120
 OY 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYGVRIODAGVLLYSQVLFQDVTFTMGQ 180
 DB 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYGVRIODAGVLLYSQVLFQDVTFTMGQ 180
 OY 181 VVSREGQGRQETLFRICIRSMPSHPDRAVNSCYAGVFHLHGDIILSVIIPARAKLNLSP 240
 DB 181 VVSREGQGRQETLFRICIRSMPSHPDRAVNSCYAGVFHLHGDIILSVIIPARAKLNLSP 240
 OY 241 HGTFLGFEVLT 250
 DB 241 HGTFLGFEVLT 250
 RESULT 14
 AAY28836
 AAY28836 standard; Protein; 247 AA.
 AC AAY28836;
 XX 17-JAN-2000 (first entry)
 DT Human TNF-related death ligand-14.
 DE
 XX Tumour necrosis factor-related death ligand-14; TRDL-14; cytokine;
 KM TNF alpha; Fas ligand; FasL; TNF-related apoptosis-inducing ligand;
 KM TRAIL; cellular apoptosis; transcription factor; NF kappa B; cancer;
 KM autoimmune disease; viral infection; antagonist; AIDS; probe; primer;
 KM neurodegenerative disease; myelodysplastic disease; lechaemic injury;
 KW chromosome localisation; antibody.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 1..23
 FT /label= N-terminal_cytoplasmic_domain
 FT Domain 24..52
 FT /label= Transmembrane_domain
 FT Domain 53..247
 FT /label= C-terminal_extracellular_domain
 XX
 XX WO950416-A1.
 XX
 XX 07-OCT-1999.
 XX
 XX 21-SEP-1998; 98WO-US18506.
 XX
 XX 30-SEP-1997; 97US-0060475.
 XX
 XX (PHAA) PHARMACIA & UPJOHN CO.
 XX
 XX PI Bienkowski MJ, Jones DA, Mills CJ;
 XX
 XX WPI: 1999-610854/52.
 XX N-PSDB: AAX90911.
 XX
 XX New nucleic acid used for promotion or inhibition of apoptosis, e.g.
 PT for treating cancer -
 XX
 XX PS Claim 1; Fig 4; 70pp; English.
 XX
 XX The present sequence is tumour necrosis factor (TNF)-related death
 CC ligand-14 (TRDL-14), that belongs to cytokine family. It shows 17%, 17%
 CC and 12% sequence homology to the C-terminal domains of TNF alpha, Fas
 CC ligand (FasL) and TNF-related apoptosis-inducing ligand (TRAIL)
 CC respectively. It can activate cellular apoptosis and transcription factor
 CC NF kappa B and can be used for treating conditions associated with
 CC inadequate levels of apoptosis, like cancer, autoimmune disease and viral
 CC infections. TRDL antagonist can be used to reduce apoptosis levels in

CC conditions like, AIDS, neurodegenerative diseases, myelodysplastic
 CC disease and ischaemic injury. TRDL gene can be used for chromosome
 CC localisation and as probe or primer for detecting TRDL nucleic acid or
 CC cells that express TRDL. Antibodies generated against TRDL are useful for
 CC detecting TRDL expression.
 XX
 XX Sequence 247 AA;
 S0
 Query Match 98.4%; Score 246; DB 20; Length 247;
 Best Local Similarity 100.0%; Pred. No. 1.6e-230;
 Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MPASSPFLAPKGPNGGVPREPALSVALMISGAAIGAVACAMALLTQOTELQSLRR 60
 DB 1 MPASSPFLAPKGPNGGVPREPALSVALMISGAAIGAVACAMALLTQOTELQSLRR 60
 OY 61 EVSRLQGTGSPONGEGYPMQSLPEQSSDPALEAENGERSRKRAVLTQKKQKHSVHL 120
 DB 61 EVSRLQGTGSPONGEGYPMQSLPEQSSDPALEAENGERSRKRAVLTQKKQKHSVHL 120
 OY 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYGVRIODAGVLLYSQVLFQDVTFTMGQ 180
 DB 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYGVRIODAGVLLYSQVLFQDVTFTMGQ 180
 OY 181 VVSREGQGRQETLFRICIRSMPSHPDRAVNSCYAGVFHLHGDIILSVIIPARAKLNLSP 240
 DB 181 VVSREGQGRQETLFRICIRSMPSHPDRAVNSCYAGVFHLHGDIILSVIIPARAKLNLSP 240
 OY 241 HGTFLG 246
 DB 241 HGTFLG 246
 RESULT 15
 AAB62327
 ID AAB62327 standard; Protein; 247 AA.
 XX
 XX AAB62327;
 XX
 XX 29-JUN-2001 (first entry)
 DT Human TRDL-1gamma polypeptide.
 DE
 XX Tumour necrosis factor related death ligand-1gamma; TRDL-1gamma; TRDL;
 KW cell death; apoptosis; human.
 XX
 XX Homo sapiens.
 OS
 XX WO200125256-A2.
 XX
 XX 12-APR-2001.
 XX
 XX 06-OCT-2000; 2000WO-US27868.
 XX
 XX 06-OCT-1999; 99US-0157913.
 XX
 XX (UTAH) UNIV UTAH RES FOUND.
 XX
 XX PI Jones D, Manos E;
 XX
 XX WPI: 2001-281728/29.
 XX N-PSDB: AAF57680.
 XX
 XX Isolated and purified polynucleotide encoding human tumor necrosis
 PT factor related death ligand (TRDL)-1 gamma useful for identifying
 PT agents that inhibit or enhance TRDL-1 gamma mediated induction of
 PT apoptosis -
 XX
 XX PS Claim 1; Page 34-36; 39pp; English.
 XX
 XX This represents a human tumour necrosis factor related death
 CC ligand-1gamma (TRDL-1gamma). The TRDL-1gamma polypeptide can be
 CC expressed by standard recombinant methodology. TRDL-1gamma stimulates

CC Tumor cell death. It is useful for identifying agents capable of
 CC inhibiting or enhancing TRAIL-gamma mediated induction of apoptosis.
 CC Sequence 247 AA;

Query Match 98.4%; Score 246; DB 22; Length 247;
 Best Local Similarity 100.0%; Pred. No. 1.6e-230;
 Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPASSPFLAPKPPGNMGCPVREPALSVLWLSGVALGAVACAMALLTQOTELQSLRR 60
 DB 1 MPASSPFLAPKPPGNMGCPVREPALSVLWLSGVALGAVACAMALLTQOTELQSLRR 60
 QY 61 EVSRLQGTGSPQNGEGYPMQSLPEQSSDALEAMENGERSRRRAVLTQKKQKSHVHL 120
 DB 61 EVSRLQGTGSPQNGEGYPMQSLPEQSSDALEAMENGERSRRRAVLTQKKQKSHVHL 120
 QY 121 VPINATSKDDSDVTEVMQOPALRRRGLOAQGYRIGDAGVLLYSQVLPDVTFTMGQ 180
 DB 121 VPINATSKDDSDVTEVMQOPALRRRGLOAQGYRIGDAGVLLYSQVLPDVTFTMGQ 180
 QY 181 VVSREGQROETLFRGIRSMPSHPDRAVNSCYSAVPHLQGDILSVIIPRRAKLNLS 240
 DB 181 VVSREGQROETLFRGIRSMPSHPDRAVNSCYSAVPHLQGDILSVIIPRRAKLNLS 240
 QY 241 HGTFLG 246
 DB 241 HGTFLG 246

RESULT 16
 ID AAY22225
 AC AAY22225; standard; Protein; 205 AA.

DT 16-SEP-1999 (first entry)
 DE Human TNF α protein sequence.
 XX
 KM TNF α : human; TNFR superfamily; tumour necrosis factor ligand; TNF;
 KM tumour necrosis factor receptor; TNFR superfamily; cell proliferation;
 KM cell differentiation; cytokine production; immunoglobulin; hyperplasia;
 KM apoptosis inducer; activated T cell; autoimmune disease; inhibitor;
 KM myasthenia gravis; insulin-dependent diabetes mellitus; endotoxin shock;
 KM rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;
 KM tumour; proliferative disorder; neoplasia; dysplasia; immunocompetence;
 KM lymphoid organogenesis; bacterial resistance; contact hypersensitivity;
 KM delayed type sensitivity; therapy.

OS Homo sapiens.
 XX
 PN WO9933980-A2.
 XX
 PD 08-JUL-1999.
 XX
 PF 22-DEC-1998; 98WO-US27474.
 XX
 PR 16-DEC-1998; 98US-0212270.
 XX
 PR 30-DEC-1997; 97US-0068959.
 XX
 PA (CHIR) CHIRON CORP.
 PI Kaasam A, Lamson G, Pot D, Tribouley C;
 DR MPI: 1999-405508/34.
 DR N-PSDB; AAX84624.

PT New tumour necrosis factor ligands, useful for induction of cell
 death and/or proliferation of cells
 XX
 PS Claim 13; Page 63; 69pp; English.

CC This sequence is the tumour necrosis factor (TNF) ligand family
 CC protein of the invention, designated TNF α . The TNF proteins play
 CC regulatory roles in cell proliferation and/or differentiation, e.g. they
 CC can induce production of cytokines, immunoglobulins, etc. A variety of
 CC diseases can be treated by modulating the activity of TNF proteins,
 CC e.g. they can induce apoptosis of activated T cells but rescue resting
 CC T cells from apoptosis. TNF polypeptides can therefore be used to treat
 CC autoimmune diseases, such as myasthenia gravis, insulin-dependent
 CC diabetes mellitus, rheumatoid arthritis, multiple sclerosis, and systemic
 CC lupus erythematosus. TNF proteins also have tumour stimulating
 CC properties, so tumours can be treated by inhibiting the expression or
 CC activity of TNF. Other proliferative disorders, such as neoplasias,
 CC dysplasias, and hyperplasias can also be treated using TNF inhibitors.
 CC The TNF polypeptides and polynucleotides can also be used to enhance or
 CC decrease TNF activity, thus providing therapeutic benefits such as
 CC induction of cell death, lymphoid organogenesis, or host bacterial
 CC resistance, and inhibition of endotoxin shock, contact hypersensitivity,
 CC delayed type sensitivity or immunocompetence of a transplant recipient.
 CC Tumour necrosis factor (TNF) and its receptors play a major role in host
 CC defence and immunosurveillance. As such, there is a need to identify new
 CC members of TNF families. This invention provides this need.

Query Match 80.8%; Score 202; DB 20; Length 205;
 Best Local Similarity 100.0%; Pred. No. 7.1e-188;
 Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 LTOOTELQSLREVSRLQGTGSPQNGEGYPMQSLPEQSSDALEAMENGERSRRRAVLT 108
 DB 4 LTOOTELQSLREVSRLQGTGSPQNGEGYPMQSLPEQSSDALEAMENGERSRRRAVLT 63
 QY 109 QKKQKSHVHLVPINATSKDDSDVTEVMQOPALRRRGLOAQGYRIGDAGVLLYSQ 168
 DB 64 QKKQKSHVHLVPINATSKDDSDVTEVMQOPALRRRGLOAQGYRIGDAGVLLYSQ 123
 QY 169 VLPDVTFTMGQVVSREGQROETLFRGIRSMPSHPDRAVNSCYSAVPHLQGDILSVI 228
 DB 124 VLPDVTFTMGQVVSREGQROETLFRGIRSMPSHPDRAVNSCYSAVPHLQGDILSVI 183
 QY 229 IPRRAKLNLSPHGTFTGFKVL 250
 DB 184 IPRRAKLNLSPHGTFTGFKVL 205

RESULT 17
 ID AAU99508
 AC AAU99508; standard; Protein; 233 AA.

DT 07-OCT-2002 (first entry)
 DE Human tumour necrosis factor (TNF) delta #1.
 XX
 KM Human; tumour necrosis factor; TNF delta; pulmonary system disorder;
 KM immunoglobulin production; B-cell proliferation; immune system disorder;
 KM autoimmune disease; cancer; lymphoproliferative disorder; pain;
 KM microbial infection; parasitic infection; bone disease; atherosclerosis;
 KM cardiovascular disorder; neurodegenerative disease; wound healing;
 KM graft versus host disease; haematopoietic cell disorder; nephritis;
 KM inflammatory disorder; mucous membrane disorder; dermatological;
 KM immunosuppressive; cytostatic.

OS Homo sapiens.
 XX
 PN US2002064829-A1.
 XX
 PD 30-MAY-2002.

PF 14-JUN-2001; 2001US-0879919.
 XX
 PR 14-MAR-1996; 96US-016812P.

PR 15-JUN-2000; 2000US-211537P.
 PR 23-OCT-2000; 2000US-241952P.
 PR 13-DEC-2000; 2000US-254875P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 23-MAR-2001; 2001US-277978P.
 PR 25-MAY-2001; 2001US-293499P.
 PR 12-MAR-1997; 97US-0815783.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Yu G, Ni J, Gentz RL, Dillon PJ;

XX WPI; 2002-556722/59.

DR N-PSDB; ABK86863.

PT Novel human multifactoric tumour necrosis factor delta or epsilon protein
 PT useful for treating disease or disorder of immune system such as
 PT autoimmune disease, immunodeficiency, or cancer of immune system -

XX Claim 1; Fig 1; 143pp; English.

CC The present invention relates to the isolation of human tumour necrosis
 CC factor (TNF) delta and TNF epsilon proteins, and the polynucleotide
 CC sequences encoding them. The proteins are useful for modulating
 CC immunoglobulin production or for modulating proliferation of B-cells.
 CC The sequences of the invention are useful for treating diseases or
 CC disorders of the immune system. Such disorders include autoimmune
 CC diseases (e.g. systemic lupus erythematosus (SLE), acquired
 CC immunodeficiency syndrome (AIDS)), cancers of the immune system
 CC (e.g. chronic lymphocytic leukaemia (CLL), multiple myeloma,
 CC non-Hodgkin's lymphoma or Hodgkin's disease), lymphoproliferative
 CC disorders, microbial infections (e.g. viral, bacterial), parasitic
 CC infections, nephritis, bone disease (e.g. osteoporosis), atherosclerosis,
 CC pain, cardiovascular disorders (e.g. myocardial infarction, stroke),
 CC neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's
 CC disease), graft versus host disease, wound healing, haematopoietic cell
 CC disorders (e.g. anaemia), inflammatory disorders (e.g. asthma),
 CC diseases or disorders associated with various mucous membranes of the
 CC body (e.g. mucositis), and disorders of the pulmonary system. The
 CC proteins are also useful as a vaccine adjuvant that enhances immune
 CC responsiveness to specific antigens. The present sequence represents
 CC human TNF delta #1.

XX Sequence 233 AA;

Query Match 73.2%; Score 183; DB 23; Length 233;

Best Local Similarity 100.0%; Pred. No. 2.3e-169; Indels 0; Gaps 0;

Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 TCGPSQNGEGYPMQSLPEQSSDALEAMNGERSRKRAVLTOKQKQSHVLHPINATS 127
 DB 51 TCGPSQNGEGYPMQSLPEQSSDALEAMNGERSRKRAVLTOKQKQSHVLHPINATS 110
 QY 128 KDDSDVTEVMWOPALRRGSLQAGYGVRIQDAGVLLYSQVLFQDVTFTMGQVVSREGQ 187
 DB 111 KDDSDVTEVMWOPALRRGSLQAGYGVRIQDAGVLLYSQVLFQDVTFTMGQVVSREGQ 170
 QY 188 GGOETLFRICIRSMPSHPDAVNSCYAGVFLHOGDIIISVIIIPRAKLNLSPHGTFICF 247
 DB 171 GGOETLFRICIRSMPSHPDAVNSCYAGVFLHOGDIIISVIIIPRAKLNLSPHGTFICF 230
 QY 248 VKL 250
 DB 231 VKL 233

RESULT 18

AAU75402

XX AAU75402 standard; Protein; 233 AA.

DT 09-APR-2002 (first entry)

XX Tumour necrosis factor delta (TNF-delta), splicing variant #1.
 DE
 XX
 KW Tumour necrosis factor delta; TNF-delta; cytostatic; arteriosclerosis;
 KW analgesic; cerebroprotective; neurotrophic; neuroprotective; hepatotropic;
 KW immunoglobulin production; B cell proliferation; immunosuppressive;
 KW HIV; human immunodeficiency virus; autoimmune disease; immunodeficiency;
 KW Sjogren's syndrome; systemic lupus erythematosus; Hodgkin's disease;
 KW common variable immunodeficiency; CVID; non-Hodgkin's lymphoma; AIDS;
 KW acquired immunodeficiency virus; cancer; multiple myeloma; CLL;
 KW chronic lymphocytic leukaemia; lymphoproliferative disorder;
 KW bacterial infection; viral infection; osteoporosis; atherosclerosis;
 KW pain; cardiovascular disorder; stroke; allergy; Alzheimer's disease;
 KW neurodegenerative disease; inflammation; liver disease; cirrhosis;
 KW cardiomyopathy; diabetes; asthma; psoriasis; glomerulonephritis;
 KW ulcerative colitis; angiogenesis; septic shock; wound healing.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..87

FT 88..233 /label= Signal_peptide

FT /label= Mature_TNF-delta

FT /note= "Tumour necrosis factor"

FT /note= "Specifically claimed in claim 1"

FT Region 39..233

FT /note= "Specifically claimed in claim 1"

FT 59..66 /label= Conserved domain I

FT /note= "Region of high identity between TNF-delta

FT and TNF-epsilon"

FT 96..104 /label= Conserved domain II

FT /note= "Region of high identity between TNF-delta

FT and TNF-epsilon"

FT 112..121 /label= Conserved domain III

FT /note= "Region of high identity between TNF-delta

FT and TNF-epsilon"

FT 126..139 /label= Conserved domain IV

FT /note= "Region of high identity between TNF-delta

FT and TNF-epsilon"

FT 138..154 /note= "TNF family signature sequence"

FT 143..154 /label= Conserved domain V

FT /note= "Region of high identity between TNF-delta

FT and TNF-epsilon"

FT 166..176 /label= Conserved domain VI

FT /note= "Region of high identity between TNF-delta

FT and TNF-epsilon"

FT 178..183 /label= Conserved domain VII

FT /note= "Region of high identity between TNF-delta

FT and TNF-epsilon"

FT 191..195 /label= Conserved domain VIII

FT /note= "Region of high identity between TNF-delta

FT and TNF-epsilon"

FT 198..209 /label= Conserved domain IX

FT /note= "Region of high identity between TNF-delta

FT and TNF-epsilon"

FT 229..233 /label= Conserved domain XI

FT /note= "Region of high identity between TNF-delta

FT and TNF-epsilon"

FT Domain

FT Domain

FT Domain

FT Domain

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FT Domain

FT Domain

FT Domain

FT Domain

W0200196528-A2.

PD 20-DEC-2001.
 XX
 PF 14-JUN-2001; 2001WO-US19026.
 XX
 PR 15-JUN-2000; 2000US-211537P.
 PR 23-OCT-2000; 2000US-241952P.
 PR 13-DEC-2000; 2000US-254875P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 23-MAR-2001; 2001US-277978P.
 PR 25-MAY-2001; 2001US-293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 P1 Yu G, Ni J, Gentz RL, Dillon PJ, Hilbert D;
 XX WPI: 2002-130727/17.
 DR N-PSDB; ABK13401.
 XX
 PT Novel multimeric human tumour necrosis factor delta or epsilon protein
 useful for treating cancer, immune system disorders, infection,
 cardiovascular disorders, liver disease, cardiomyopathy, diabetes and
 psoriasis -

XX
 PS Claim 1; Fig 1A-B; 344pp; English.

XX
 CC The invention describes a multimeric human tumour necrosis factor (TNF)
 CC delta or epsilon protein (I). (I) or a composition containing them (II)
 CC are useful for modulating immunoglobulin production or proliferation of B
 CC cells. (I) or (II) is useful for treating a disease or disorder of the
 CC immune system, preferably an autoimmune disease (e.g. Sjogren's syndrome,
 CC systemic lupus erythematosus or common variable immunodeficiency (CVID));
 CC an immunodeficiency e.g. acquired immunodeficiency syndrome (AIDS);
 CC cancer of the immune system (e.g. Hodgkin's disease, non-Hodgkin's
 CC lymphoma, multiple myeloma and chronic lymphocytic leukaemia (CLL)); in
 CC the diagnosis and treatment or prevention of cancer, lymphoproliferative
 CC disorder, bacterial and viral infections, osteoporosis, atherosclerosis,
 CC pain, cardiovascular disorders (e.g. stroke), allergy, inflammation,
 CC neurodegenerative disease (e.g. Alzheimer's disease), liver disease (e.g.
 CC cirrhosis), cardiomyopathy, diabetes, asthma, psoriasis, septic shock,
 CC glomerulonephritis, ulcerative colitis, arteriosclerosis, for promoting
 CC angiogenesis and wound healing; as a diagnostic research reagent; as an
 CC agent to target and kill cells expressing a TNFdelta and/or TNFepsilon
 CC receptor; in apoptosis of transformed cell lines; mediation of cell
 CC activation and proliferation; and as an immunogen to produce (II). (II)
 CC is useful to purify, detect and target (I), for measuring levels of (I)
 CC in biological samples, for immunophenotyping samples, and to treat.
 CC inhibit or prevent diseases and disorders associated with aberrant
 CC expression and/or activity of (I). This is the amino acid sequence of
 CC human tumour necrosis factor delta (TNF-delta) splicing variant #1,
 CC described in the method of the invention.

XX
 SO Sequence 233 AA;

Query Match 73.2%; Score 183; DB 23; Length 233;
 Best Local Similarity 100.0%; Pred. No. 2.3e-169;

Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 TGGPSONGEGYPMOSLPDESSDLEAWENGERSRKRRAVLTKOKKHSHVHLVPINATS 127
 DB 51 TGGPSONGEGYPMOSLPDESSDLEAWENGERSRKRRAVLTKOKKHSHVHLVPINATS 110
 QY 128 KDDSDVTEVMQPALRRGRGLQAGYGVRIODAGVYLLYSQVLPDVTFTMGQVVSREGQ 187
 DB 111 KDDSDVTEVMQPALRRGRGLQAGYGVRIODAGVYLLYSQVLPDVTFTMGQVVSREGQ 170
 QY 188 GHOETLFFCIRSMPSHPDRAYNSCYSAVFHLHOGDILSVIIPRAKLNLSPHGTPLGF 247
 DB 171 GHOETLFFCIRSMPSHPDRAYNSCYSAVFHLHOGDILSVIIPRAKLNLSPHGTPLGF 230

QY 248 VKL 250
 DB 231 VKL 233

RESULT 19

AAV05745
 ID AAV05745 standard; Protein; 250 AA.

XX
 AC AAV05745;

DT 19-JUL-1999 (first entry)

XX Tumour necrosis factor receptor ligand TL3.

DE Tumour necrosis factor receptor ligand TL3; agonist;
 KM antagonist; screening; human; cancer; AIDS; Alzheimer's disease;
 KM inflammation; arthritis; septicemia; autoimmune disease;
 KM psoriasis; inflammatory bowel disease; transplant rejection;
 KM graft versus host disease; infection; stroke; ischaemia;
 KM acute respiratory disease syndrome; retinosis; brain injury;
 KM bone disease; atherosclerosis; therapy.

XX Homo sapiens.

OS
 PN EP911633-A1.

XX 28-APR-1999.

PF 02-OCT-1998; 98EP-0203332.

PR 08-OCT-1997; 97US-0061334.

XX (SMIK) SMITHKLINE BEECHAM CORP.

PI McDonnell PC, Young PR, Zou J;

XX WPI: 1999-246560/21.

DR N-PSDB; AAX25380.

PT Identifying agonists and antagonists of tumor necrosis factor
 PT related receptors TR1, TR3 and TR5, and of ligand TL3, useful for
 PT treatment of cancer, AIDS, Alzheimer's disease, bone disease etc
 XX
 PS Disclosure; Page 14-15; 23pp; English.

XX
 CC The present sequence represents tumour necrosis factor receptor
 CC (TNFR) ligand TL3, which acts as a ligand for TNFRs TR1, TR3 and
 CC TR5 (see AAV05742-44). TR1, TR3, TR5 and TL3 are used in claimed
 CC methods of identifying agonists and antagonists, i.e. compounds
 CC that bind to the receptors or ligand, and which activate (agonist)
 CC or inhibit activation of (antagonists) TR1, TR3, TR5 or TL3. A
 CC screening kit for identifying agonists, antagonists, ligands,
 CC receptors, substrates, enzymes etc. for TR1, TR3, TR5 or TL3
 CC polypeptides is provided. The agonists and antagonists are
 CC useful for treatment of chronic and acute inflammation, arthritis,
 CC septicemia, autoimmune disease e.g. inflammatory bowel disease,
 CC psoriasis, transplant rejection, graft versus host disease,
 CC infection, stroke, ischaemia, acute respiratory disease syndrome,
 CC retinosis, brain injury, AIDS, bone diseases, cancer (e.g.
 CC lymphoproliferative disorders), atherosclerosis and Alzheimer's
 CC disease, etc., caused by imbalance of TR1, TR3, TR5 or TL3.

XX
 SO Sequence 250 AA;

Query Match 73.2%; Score 183; DB 20; Length 250;

Best Local Similarity 100.0%; Pred. No. 2.4e-169;

Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 TGGPSONGEGYPMOSLPDESSDLEAWENGERSRKRRAVLTKOKKHSHVHLVPINATS 127
 DB 68 TGGPSONGEGYPMOSLPDESSDLEAWENGERSRKRRAVLTKOKKHSHVHLVPINATS 127
 QY 128 KDDSDVTEVMQPALRRGRGLQAGYGVRIODAGVYLLYSQVLPDVTFTMGQVVSREGQ 187
 DB 128 KDDSDVTEVMQPALRRGRGLQAGYGVRIODAGVYLLYSQVLPDVTFTMGQVVSREGQ 187

QY 188 GROETLFRICIRSMPSHPDRAVNSCYSAGVFLHOGDILSVIIPRAKLNLSPHGTFLGCF 247
 DB 188 GAGETLFRICIRSMPSHPDRAVNSCYSAGVFLHOGDILSVIIPRAKLNLSPHGTFLGCF 247
 QY 248 VKL 250
 DB 248 VKL 250

RESULT 20
 AAU99510
 ID AAU99510 standard; Protein; 250 AA.
 AC AAU99510;
 XX 07-OCT-2002 (first entry)
 DT
 DE Human tumour necrosis factor (TNF) delta #2.
 XX
 XX Human; tumour necrosis factor; TNF delta; pulmonary system disorder;
 XX immunoglobulin production; B-cell proliferation; immune system disorder;
 XX autoimmune disease; cancer; lymphoproliferative disorder; pain;
 XX microbial infection; parasitic infection; bone disease; atherosclerosis;
 XX cardiovascular disorder; neurodegenerative disease; wound healing;
 XX graft versus host disease; haematopoietic cell disorder; nephritis;
 XX inflammatory disorder; mucous membrane disorder; dermatological;
 XX immunosuppressive; cytostatic.
 OS Homo sapiens.
 XX
 XX US2002064829-A1.
 XX
 PD 30-MAY-2002.
 XX
 XX 14-JUN-2001; 2001US-0879919.
 PF
 XX 14-MAR-1996; 96US-016812P.
 XX 15-JUN-2000; 2000US-211537P.
 PR 23-OCT-2000; 2000US-241952P.
 PR 13-DEC-2000; 2000US-254875P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 23-MAR-2001; 2001US-277978P.
 PR 25-MAY-2001; 2001US-293499P.
 PR 12-MAR-1997; 97US-0815783.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 PI Yu G, Ni J, Gentz RL, Dillon PJ;
 DR WPI; 2002-556722/59.
 XX N-PSDB; ABR86863.
 PT Novel human multimeric tumour necrosis factor delta or epsilon protein
 PT useful for treating disease or disorder of immune system such as
 PT autoimmune disease, immunodeficiency, or cancer of immune system -
 PS
 XX Claim 1; Fig 6; 143pp; English.

The present invention relates to the isolation of human tumour necrosis factor (TNF) delta and TNF epsilon proteins, and the polynucleotide sequences encoding them. The proteins are useful for modulating immunoglobulin production or for modulating proliferation of B-cells. The sequences of the invention are useful for treating diseases or disorders of the immune system. Such disorders include autoimmune diseases (e.g. systemic lupus erythematosus (SLE), acquired immunodeficiency syndrome (AIDS)), cancers of the immune system (e.g. chronic lymphocytic leukaemia (CLL), multiple myeloma, non-Hodgkin's lymphoma or Hodgkin's disease), lymphoproliferative disorders, microbial infections (e.g. viral, bacterial), parasitic infections, nephritis, bone disease (e.g. osteoporosis), atherosclerosis, pain, cardiovascular disorders (e.g. myocardial infarction, stroke), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), graft versus host disease, wound healing, haematopoietic cell

CC disorders (e.g. anaemia), inflammatory disorders (e.g. asthma),
 CC diseases or disorders associated with various mucous membranes of the
 CC body (e.g. mucositis), and disorders of the pulmonary system. The
 CC proteins are also useful as a vaccine adjuvant that enhances immune
 CC responsiveness to specific antigens. The present sequence represents
 CC human TNF delta #2.
 CC
 XX
 SQ Sequence 250 AA;
 Query Match 73.2%; Score 183; DB 23; Length 250;
 Best Local Similarity 100.0%; Pred. No. 2, 4e-169;
 Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 TGGPSONGEGYPMQSLPEQSSDALEAMENGERSRRRAVLTKOKKQSHVHLVPINATS 127
 DB 68 TGGPSONGEGYPMQSLPEQSSDALEAMENGERSRRRAVLTKOKKQSHVHLVPINATS 127
 QY 128 KDDSPVTEVMNQPALRRRGVQAGYGVRIODAGVYLLYSGLFQDVFTFMGOVVSREGQ 187
 DB 128 KDDSPVTEVMNQPALRRRGVQAGYGVRIODAGVYLLYSGLFQDVFTFMGOVVSREGQ 187
 QY 188 GROETLFRICIRSMPSHPDRAVNSCYSAGVFLHOGDILSVIIPRAKLNLSPHGTFLGCF 247
 DB 188 GROETLFRICIRSMPSHPDRAVNSCYSAGVFLHOGDILSVIIPRAKLNLSPHGTFLGCF 247
 QY 248 VKL 250
 DB 248 VKL 250

RESULT 21
 AAU75406
 ID AAU75406 standard; Protein; 250 AA.
 XX
 AC AAU75406;
 XX
 DT 09-APR-2002 (first entry)
 DE
 XX Tumour necrosis factor delta (TNF-delta), splicing variant #2.
 XX
 XX Tumour necrosis factor delta; TNF-delta; cytostatic; atherosclerosis;
 XX analgesic; cerebroprotective; neurotropic; neuroprotective; hepatotropic;
 XX immunoglobulin production; B cell proliferation; immunosuppressive;
 XX HIV; human immunodeficiency virus; autoimmune disease; immunodeficiency;
 XX Sjogren's syndrome; systemic lupus erythematosus; Hodgkin's disease;
 XX common variable immunodeficiency; CVID; cancer; non-Hodgkin's lymphoma;
 XX AIDS; acquired immunodeficiency virus; multiple myeloma; CLL;
 XX chronic lymphocytic leukaemia; atherosclerosis; bacterial infection;
 XX lymphoproliferative disorder; viral infection; osteoporosis; pain;
 XX cardiovascular disorder; stroke; allergy; Alzheimer's disease;
 XX neurodegenerative disease; inflammation; liver disease; cirrhosis;
 XX cardiomyopathy; diabetes; asthma; psoriasis; glomerulonephritis;
 XX ulcerative colitis; angiogenesis; septic shock; wound healing.
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT 1..104
 FT /label= Signal_peptide
 FT Protein 105..250
 FT /label= Mature_TNF-delta
 FT /note= "Tumour necrosis factor"
 FT Domain 76..83
 FT /label= Conserved domain I
 FT /note= "Region of high identity between TNF-delta
 FT and TNF-epsilon"
 FT Domain 113..121
 FT /label= Conserved domain II
 FT /note= "Region of high identity between TNF-delta
 FT and TNF-epsilon"
 FT Domain 129..138
 FT /label= Conserved domain III
 FT /note= "Region of high identity between TNF-delta
 FT and TNF-epsilon"

FT	Domain	143..154	and TNF-epsilon"
FT	Domain	/label= "Conserved domain IV	
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	155..171	and TNF-epsilon"
FT	/note= "TNF family signature sequence"		
FT	Domain	160..171	
FT	/label= "Conserved domain V		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	183..193	and TNF-epsilon"
FT	/label= "Conserved domain VI		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	196..201	and TNF-epsilon"
FT	/label= "Conserved domain VII		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	208..212	and TNF-epsilon"
FT	/label= "Conserved domain VIII		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	215..226	and TNF-epsilon"
FT	/label= "Conserved domain IX		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	229..236	and TNF-epsilon"
FT	/label= "Conserved domain X		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	246..250	and TNF-epsilon"
FT	/label= "Conserved domain XI		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	255..260	and TNF-epsilon"
FT	/label= "Conserved domain XII		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	265..270	and TNF-epsilon"
FT	/label= "Conserved domain XIII		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	275..280	and TNF-epsilon"
FT	/label= "Conserved domain XIV		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	285..290	and TNF-epsilon"
FT	/label= "Conserved domain XV		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	295..300	and TNF-epsilon"
FT	/label= "Conserved domain XVI		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	305..310	and TNF-epsilon"
FT	/label= "Conserved domain XVII		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	315..320	and TNF-epsilon"
FT	/label= "Conserved domain XVIII		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	325..330	and TNF-epsilon"
FT	/label= "Conserved domain XIX		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	335..340	and TNF-epsilon"
FT	/label= "Conserved domain XX		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	345..350	and TNF-epsilon"
FT	/label= "Conserved domain XXI		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	355..360	and TNF-epsilon"
FT	/label= "Conserved domain XXII		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	365..370	and TNF-epsilon"
FT	/label= "Conserved domain XXIII		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	375..380	and TNF-epsilon"
FT	/label= "Conserved domain XXIV		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	385..390	and TNF-epsilon"
FT	/label= "Conserved domain XXV		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	395..400	and TNF-epsilon"
FT	/label= "Conserved domain XXVI		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	405..410	and TNF-epsilon"
FT	/label= "Conserved domain XXVII		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	415..420	and TNF-epsilon"
FT	/label= "Conserved domain XXVIII		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	425..430	and TNF-epsilon"
FT	/label= "Conserved domain XXIX		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	435..440	and TNF-epsilon"
FT	/label= "Conserved domain XXX		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	445..450	and TNF-epsilon"
FT	/label= "Conserved domain XXXI		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	455..460	and TNF-epsilon"
FT	/label= "Conserved domain XXXII		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	465..470	and TNF-epsilon"
FT	/label= "Conserved domain XXXIII		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	475..480	and TNF-epsilon"
FT	/label= "Conserved domain XXXIV		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	485..490	and TNF-epsilon"
FT	/label= "Conserved domain XXXV		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	495..500	and TNF-epsilon"
FT	/label= "Conserved domain XXXVI		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	505..510	and TNF-epsilon"
FT	/label= "Conserved domain XXXVII		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	515..520	and TNF-epsilon"
FT	/label= "Conserved domain XXXVIII		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	525..530	and TNF-epsilon"
FT	/label= "Conserved domain XXXIX		
FT	/note= "Region of high identity between TNF-delta		
FT	Domain	535..540	and TNF-epsilon"
FT	/label= "Conserved domain XXXX		
FT</			

CC	disorder,bacterial and viral infections, osteoporosis, atherosclerosis,
CC	pain, cardiovascular disorders (e.g. stroke), allergy, inflammation,
CC	neurodegenerative disease (e.g. Alzheimer's disease), liver disease (e.g.
CC	cirrhosis), cardiomyopathy, diabetes, asthma, psoriasis, septic shock,
CC	glomerulonephritis, ulcerative colitis, arteriosclerosis; for promoting
CC	angiogenesis and wound healing; as a diagnostic research reagent; as an
CC	agent to target and kill cells expressing a TNFdelta and/or TNFepilson
CC	receptor; in apoptosis of transformed cell lines; mediation of cell
CC	activation and proliferation; and as an immunogen to produce (11). (11)
CC	is useful to purify, detect and target (1), for measuring levels of (1)
CC	in biological samples, for immunophenotyping samples, and to treat,
CC	inhibit or prevent diseases and disorders associated with aberrant
CC	expression and/or activity of (1). This is the amino acid sequence of
CC	human tumour necrosis factor delta (TNF-delta) splicing variant #2,
CC	described in the method of the invention.
CC	
XX	
S0	Sequence 250 AA;
Query Match	73.2%; Score 183; DB 23; Length 250;
Best Local Similarity	100.0%; Pred. No. 2.4e-169;
Matches 183; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Oy	68 TGGSGNGEGYPMOSLPPQSSDALAEWNGRSRKRRAVLTKOKKQHSVLHLVPINATS 127
Db	68 TGGSGNGEGYPMOSLPPQSSDALAEWNGRSRKRRAVLTKOKKQHSVLHLVPINATS 127
Oy	128 KDDSDYEVMMQPALRRGRGLQAQGYGVRIODAGVYLLYSQVLFQDYFTFMGVVSRQ 187
Db	128 KDDSDYEVMMQPALRRGRGLQAQGYGVRIODAGVYLLYSQVLFQDYFTFMGVVSRQ 187
Oy	188 GROETLFFCICISMSHPDRAYNSCYSAQGVFHLHOGDILSVIIPARAKLNISPHTGLGF 247
Db	188 GROETLFFCICISMSHPDRAYNSCYSAQGVFHLHOGDILSVIIPARAKLNISPHTGLGF 247
Oy	248 VKL 250
Db	248 VKL 250
RESULT 22	
AA09551	
ID	AA09551 standard; Protein; 233 AA.
AC	AA09551;
XX	
DT	21-JUL-1999 (first entry)
XX	
DE	Human TRAILLK-3 protein.
XX	
KW	Human; TRAILLK-3; TNF ligand family; tumour necrosis factor; Apo-2L;
KW	cancerous growth; breast cancer; feed additive.
XX	
OS	Homo sapiens.
XX	
PN	EP919620-A2.
PD	02-JUN-1999.
XX	
PF	25-NOV-1998; 98EP-0309670.
XX	
PR	11-AUG-1998; 98US-0096171.
PR	26-NOV-1997; 97US-0066576.
XX	
PA	(EHLIL) LILLY & CO ELI.
P1	' Song HY;
DR	WPI; 1999-304824/26.
DR	N-PSDB; AAX56316.
XX	
PT	New Tumour Necrosis Factor Family Ligand, useful for treatment of
XX	cancer

PS Claim 1; Page 19-20; 21pp; English.

XX The present sequence represents human TRAILK-3 protein (I) which is a
CC membrane-bound protein that is a member of the Tumour Necrosis Factor
CC (TNF) ligand family. TRAILK-3 (I) is useful for identifying compounds and
CC that bind it, by observing interaction between candidate compounds and
CC (I). TRAILK-3 (I) is also useful in pharmaceutical compositions,
CC and for treatment of cancer patients (especially breast cancer) in need
CC of TRAILK-3 protein. TRAILK-3 polynucleotide fragments are useful as
CC diagnostic tools to detect polymorphisms in DNA samples, for detecting
CC and isolating homologues of TRAILK-3, and as primers for amplification
CC and alteration of native sequences. The fragments are also useful as
CC antigens for producing antibodies to (I), which are useful for detecting
CC the presence of TRAILK-3 and for screening for modulators of TRAILK-3.
CC TRAILK-3 (I) is useful for developing new compounds for feed additives.

XX Sequence 233 AA;

Query Match 61.6%; Score 154; DB 20; Length 233;

Best Local Similarity 100.0%; Pred. No. 3.3e-141; Mismatches 0; Indels 0; Gaps 0;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 GERSRRRAVLTOKOKHSHLVLPINATSKDSDVTEVMQPALRRGRGLQAGGYVR 156
DB 80 GERSRRRAVLTOKOKHSHLVLPINATSKDSDVTEVMQPALRRGRGLQAGGYVR 139

QY 157 IQDAGVYLISQVLFQDVTFTMGQVSRREGGROETLFRICRSMPSHPDRAYNSCYSAGV 216
DB 140 IQDAGVYLISQVLFQDVTFTMGQVSRREGGROETLFRICRSMPSHPDRAYNSCYSAGV 199

QY 217 FHLHGGDILSVIIPARA KNLNSPHGTFGLGFVKL 250
DB 200 FHLHGGDILSVIIPARA KNLNSPHGTFGLGFVKL 233

RESULT 23

AAW93588 standard; Protein; 250 AA.

AC AAW93588;

DT 18-JUN-1999 (first entry)

DE Human TNRL1-beta protein.

KM Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KM developmental abnormality; gestational abnormality; prostate cancer;
KM APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KM cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KM apoptosis; human; TNRL1-beta.

OS Homo sapiens.

PN WO9911791-A2.

PD 11-MAR-1999.

PF 04-SEP-1998; 98WO-US18393.

PR 05-SEP-1997; 97US-0924634.

PA (UNIW) UNIV WASHINGTON.

PI Chaudhary PM;

DR WPI; 1999-205191/17.

DR N-PSDB; AAX23422.

PT New Tumour Necrosis Factor family receptor polypeptides and ligands -
PT useful for diagnosis and treatment of prostate cancer and
PT developmental or gestational abnormalities

PS Claim 35; Fig 12A; 156pp; English.

XX This invention describes isolated Tumour Necrosis Factor (TNF) family
CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
CC their active fragments. APO4 is useful for diagnosing prostate cancer
CC by determining levels of APO4 in an individual. Prostate cancer can also
CC be treated using APO4 selective binding agents linked to a therapeutic
CC moiety. APO4 polypeptides are also useful for identifying selective
CC binding agents, useful in diagnosis/treatment of disease by binding of
CC agents to the polypeptide/active fragment which is extracellular, or
CC expressed on the cell surface. The binding is preferably performed in
CC vivo. APO4 polypeptides/active fragments are also useful for screening
CC for agonists and antagonists by binding and observing the change in APO4
CC activity. Effective pharmacological agents useful in diagnosis or
CC treatment of disease are also identified using APO4 polypeptides/active
CC fragments and APO4 signal transducer molecules that specifically interact
CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC activity. The method is performed in vivo or in vitro. APO polypeptides
CC are all useful as immunogens for preparing antibodies. APO4 is also
CC useful for diagnosis/treatment of developmental or gestational
CC abnormalities. APO8 was transfected to human breast carcinoma cell line
CC MCF-7, and induced apoptosis.

XX Sequence 250 AA;

Query Match 61.6%; Score 154; DB 20; Length 250;

Best Local Similarity 100.0%; Pred. No. 3.5e-141; Mismatches 0; Indels 0; Gaps 0;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 GERSRRRAVLTOKOKHSHLVLPINATSKDSDVTEVMQPALRRGRGLQAGGYVR 156
DB 97 GERSRRRAVLTOKOKHSHLVLPINATSKDSDVTEVMQPALRRGRGLQAGGYVR 156

QY 157 IQDAGVYLISQVLFQDVTFTMGQVSRREGGROETLFRICRSMPSHPDRAYNSCYSAGV 216
DB 157 IQDAGVYLISQVLFQDVTFTMGQVSRREGGROETLFRICRSMPSHPDRAYNSCYSAGV 216

QY 217 FHLHGGDILSVIIPARA KNLNSPHGTFGLGFVKL 250
DB 217 FHLHGGDILSVIIPARA KNLNSPHGTFGLGFVKL 250

RESULT 24

AA79670 standard; Protein; 250 AA.

AC AA79670;

DT 29-AUG-2000 (first entry)

DE Human death receptor ligand-1 (DRL-1).

KM DRL-1; human; death receptor ligand-1; tumour necrosis factor;
KM TNF-gamma; TNF-like ligand; TUL; immunostimulant; immunosuppressive;
KM T-cell response; transplant rejection; graft versus host disease;
KM apoptosis.

OS Homo sapiens.

PN WO200026244-A2.

PD 11-MAY-2000.

PF 04-NOV-1999; 99WO-US25954.

PA (UNIW) UNIV WASHINGTON.

PI Chaudhary PM;

DR WPI; 1999-205191/17.

DR N-PSDB; AAX23422.

PT New Tumour Necrosis Factor family receptor polypeptides and ligands -
PT useful for diagnosis and treatment of prostate cancer and
PT developmental or gestational abnormalities

PS Claim 35; Fig 12A; 156pp; English.

PR 04-NOV-1998; 98US-0106976.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA Leonardo MJ, Wang J, Jiang D;
XX WPI: 2000-365575/31.
DR N-PSDB; AAA27732.
XX Novel nucleic acids encoding tumor necrosis factor family polypeptides
PT termed as Death Receptor ligands useful for stimulating immune response
PT and inducing apoptosis comprising a specific nucleotide sequence -
XX
XX Claim 6; Fig 1A; 80pp; English.
PS
XX The present sequence is that of human death receptor ligand 1
CC (DRL-1), a novel member of the tumour necrosis factor (TNF) family,
CC also termed TNF-gamma or TNF-like ligand (TLL). The sequence was
CC deduced from cDNA (see AAA27732) isolated from a lymphoma cell line.
CC DRL-1 is expressed as a 1.8 kb transcript in heart, placenta, lung,
CC kidney and pancreas. In the lymphoid tissue, it is expressed in
CC the peripheral lymphoid organs but not in the thymus or foetal
CC liver. The invention provides human and murine DRL polypeptides,
CC nucleic acids and antibodies. DRL-1 polypeptides are used in
CC claimed methods of stimulating an immune response and of inducing
CC apoptosis in a population of T-cells. Antibodies to DRL-1 are
CC used in claimed methods of suppressing an immune response,
CC inhibiting a T-cell response associated with transplant rejection
CC or graft versus host disease, inhibiting apoptosis in a population
CC of T cells, and of stimulating the membrane-bound form of DRL-1.
XX
XX Sequence 250 AA;
XX
XX Query Match 61.6%; Score 154; DB 21; Length 250;
XX Best Local Similarity 100.0%; Pred. No. 3.5e-141;
XX Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 97 GERSRRRAVLTQKKQSHVLAHPINATSKDSDVTEVMQPALRRGRLQAGYGV 156
XX DB 97 GERSRRRAVLTQKKQSHVLAHPINATSKDSDVTEVMQPALRRGRLQAGYGV 156
XX
XX QY 157 IODAGVYLLYSQVLFQDVTFTMGQVVSREGGREGTLPFCIRSMSPHPRAYNSCYSGV 216
XX DB 157 IODAGVYLLYSQVLFQDVTFTMGQVVSREGGREGTLPFCIRSMSPHPRAYNSCYSGV 216
XX
XX QY 217 FHLHOGDILSVIIPARAKNLSPHGTFLGFKVL 250
XX DB 217 FHLHOGDILSVIIPARAKNLSPHGTFLGFKVL 250
XX
XX RESULT 25
XX AAE15502
XX ID AAE15502 standard; Protein; 250 AA.
XX AC AAE15502;
XX DT 12-MAR-2002 (first entry)
XX XX Human APRIL G70 protein #2.
XX DE
XX XX Human; transmembrane activator and intracellular CAML interactor; TACT;
XX KM cytoskeletal; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
XX KM lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
XX KM prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
XX KM drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
XX KM Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
XX KM human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
XX KM rheumatoid arthritis; atherosclerosis; APRIL G70.
XX OS
XX XX Homo sapiens.
XX PN WO200187979-A2.
XX

PD 22-NOV-2001.
XX
XX PF 14-MAY-2001; 2001WO-US15567.
XX
XX PR 12-MAY-2000; 2000US-204039P.
XX PR 27-JUN-2000; 2000US-214591P.
XX PR 14-MAY-2001; 2001US-0214591.
XX
XX PA (AMGE-) AMGEN INC.
XX
XX PI Theill LE, Yu G;
XX
XX WPI: 2002-066686/09.
XX
XX Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor
PT family ligand -
XX
XX Disclosure; Fig 3; 94pp; English.
XX
XX PS The invention relates to a method for inhibiting TACI (transmembrane
CC activator and intracellular CAML interactor) and/or B cell maturation
CC protein (BCMA) activity in a mammal. The method comprises administering
CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis), rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human APRIL G70 protein.
XX
XX Sequence 250 AA;
XX
XX Query Match 61.6%; Score 154; DB 21; Length 250;
XX Best Local Similarity 100.0%; Pred. No. 3.5e-141;
XX Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 97 GERSRRRAVLTQKKQSHVLAHPINATSKDSDVTEVMQPALRRGRLQAGYGV 156
XX DB 97 GERSRRRAVLTQKKQSHVLAHPINATSKDSDVTEVMQPALRRGRLQAGYGV 156
XX
XX QY 157 IODAGVYLLYSQVLFQDVTFTMGQVVSREGGREGTLPFCIRSMSPHPRAYNSCYSGV 216
XX DB 157 IODAGVYLLYSQVLFQDVTFTMGQVVSREGGREGTLPFCIRSMSPHPRAYNSCYSGV 216
XX
XX QY 217 FHLHOGDILSVIIPARAKNLSPHGTFLGFKVL 250
XX DB 217 FHLHOGDILSVIIPARAKNLSPHGTFLGFKVL 250
XX
XX RESULT 26
XX AAY60542
XX ID AAY60542 standard; Protein; 260 AA.
XX AC AAY60542;
XX DT 31-JAN-2000 (first entry)
XX XX Human normal bladder tissue EST encoded protein 214.
XX DE
XX XX Human; bladder; treatment; EST; expressed sequence tag; cytoskeletal;
XX KM cancer; gene therapy.
XX

OS Homo sapiens.
 XX DE19818620-A1.
 XX
 XX 28-OCT-1999.
 XX
 XX 21-APR-1998; 98DE-1018620.
 XX PF
 XX 21-APR-1998; 98DE-1018620.
 XX PR
 XX (META-) METAGEN GES GENOMFORSCHUNG MBH.
 XX PA
 XX
 XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
 XX MPI, 1999-602416/52.
 XX DR N-PSDB; AA242229.
 XX
 PT New polypeptides and their nucleic acids, useful for treatment of
 PT bladder tumour and identification of therapeutic agents -
 XX
 XX Claim 23; Page 331; 366pp; German.
 CC This invention describes novel polypeptide fragment sequences (I) and
 CC their encoding nucleic acids (II) which are highly expressed in normal
 CC bladder tissue and have cytostatic activity. (II) are used for
 CC recombinant expression of (I) and to isolate complete genes. (I) are
 CC used to identify agents suitable for the treatment of bladder tumours,
 CC to directly treat this form of cancer (including expression from gene,
 CC therapy vectors), or are used in a preparation for cancer treatment. (I)
 CC is also used for the generation of specific antibodies. (II) are
 CC identified by assembling ESTs (expressed sequence tags) from a
 CC particular tissue type before comparison of expression patterns. This
 CC allows a significantly longer fragment of the gene to be revealed, and
 CC therefore reduces the number of failures because of ESTs from different
 CC libraries representing different parts of the same unknown gene
 CC disrupting the estimated frequency of occurrence in a particular tissue.
 CC AA50329-760591 represent protein fragments encoded by the human normal
 CC bladder tissue cDNA library derived EST fragments represented in
 CC AA21212-242248.
 XX
 XX Sequence 260 AA:
 SQ
 Query Match 61.6%; Score 154; DB 20; Length 260;
 Best Local Similarity 100.0%; Pred. No. 3.6e-141;
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 97 GERSRRRAVLTQKKQKSHVLTLPINATSKDSDVTEVMQPALRRGRGLQAQGYVR 156
 107 GERSRRRAVLTQKKQKSHVLTLPINATSKDSDVTEVMQPALRRGRGLQAQGYVR 166
 QY 157 IODAGVYLLYSQVLFQDVTFTMGQVVSREGGROETLFRICRSMSPHPRAYNSCYSAGV 216
 DB 167 IODAGVYLLYSQVLFQDVTFTMGQVVSREGGROETLFRICRSMSPHPRAYNSCYSAGV 226
 QY 217 FHLHOGDILSVIIPRARAKLNLSPHGTFLGFYKL 250
 DB 227 FHLHOGDILSVIIPRARAKLNLSPHGTFLGFYKL 260
 RESULT 27
 AAB54342
 ID AAB54342 standard; Protein; 260 AA.
 XX
 XX AAB54342;
 AC
 XX
 XX 09-MAR-2001 (first entry)
 DT
 XX
 XX Human pancreatic cancer antigen protein sequence SEQ ID NO:794.
 DE
 XX
 XX Human; pancreas; pancreatic cancer; pancreatic cancer antigen;
 KM detection; diagnosis; identification; cytostatic; neuroprotective;
 KW neoplastic; immunomodulatory; relaxant; contraceptive; gynaecological;
 KM antiinflammatory; cardiac; gene therapy; chromosome mapping;

KW linkage analysis; tissue identification; tissue typing; forensic;
 KW neutral; immune system; muscular; reproductive; gastrointestinal;
 KW pulmonary; cardiovascular; renal; proliferative.
 XX
 XX Homo sapiens.
 XX OS
 XX WO200055320-A1.
 XX PN
 XX 21-SEP-2000.
 XX PD
 XX 08-MAR-2000; 2000KO-US05989.
 XX PF
 XX 12-MAR-1999; 99US-0124270.
 XX PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX PA
 XX Rosen CA, Ruben SM;
 XX PI
 XX MPI; 2000-579444/54.
 XX DR N-PSDB; AAC99107.
 XX
 PT New nucleic acid that is a pancreatic cancer antigen for preventing,
 PT treating, or ameliorating a medical condition, particular pancreatic
 PT cancer, or for use in assays for diagnosing a pathological condition -
 XX
 XX Claim 11; Page 1235-1236; 1379pp; English.
 CC AAC98773 to AAC99231 encode the human pancreatic cancer associated
 CC proteins, called pancreatic cancer antigens, given in AAB54008 to
 CC AAB54466. The human pancreatic cancer antigens have cytostatic,
 CC neuroprotective, neotropic, immunomodulatory, relaxant, contraceptive,
 CC gynaecological, cardiac and antiinflammatory activities, and can be used
 CC in gene therapy. The polynucleotide and proteins can be used for
 CC preventing, treating, or ameliorating a medical condition or in assays
 CC for diagnosing a pathological condition or a susceptibility to one in a
 CC subject. Binding partners to the proteins and the activity of the
 CC proteins can be identified. The pancreatic cancer antigens can be used to
 CC detect, treat or prevent pancreatic disorders, especially cancer.
 CC Agonists and antagonists to the antigens can be screened for. The
 CC pancreatic cancer antigen polynucleotides can be used to design nucleic
 CC acid hybridisation probes that can be used in chromosome mapping, linkage
 CC analysis, tissue identification and/or typing and a variety of forensic
 CC and diagnostic methods. The proteins can be used to generate antibodies
 CC which are used to purify, detect and target the polypeptides, including
 CC both in vivo and in vitro diagnostic and therapeutic methods. The
 CC proteins can be used to treat or prevent neural, immune system, muscular,
 CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
 CC proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
 CC sequences used in the exemplification of the present invention.
 XX
 XX Sequence 260 AA:
 SQ
 Query Match 61.6%; Score 154; DB 21; Length 260;
 Best Local Similarity 100.0%; Pred. No. 3.6e-141;
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 97 GERSRRRAVLTQKKQKSHVLTLPINATSKDSDVTEVMQPALRRGRGLQAQGYVR 156
 DB 107 GERSRRRAVLTQKKQKSHVLTLPINATSKDSDVTEVMQPALRRGRGLQAQGYVR 166
 QY 157 IODAGVYLLYSQVLFQDVTFTMGQVVSREGGROETLFRICRSMSPHPRAYNSCYSAGV 216
 DB 167 IODAGVYLLYSQVLFQDVTFTMGQVVSREGGROETLFRICRSMSPHPRAYNSCYSAGV 226
 QY 217 FHLHOGDILSVIIPRARAKLNLSPHGTFLGFYKL 250
 DB 227 FHLHOGDILSVIIPRARAKLNLSPHGTFLGFYKL 260
 RESULT 28
 AAE15482
 ID AAE15482 standard; Protein; 248 AA.
 XX

AC AAE15482;
 XX
 XX 12-MAR-2002 (first entry)
 XX
 DE Human APRIL G70 protein #1.
 XX
 KW Human; transmembrane activator and intracellular CAML interactor; TAC1;
 KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis; APRIL G70.
 XX
 XX Homo sapiens.
 OS
 PN WO200187979-A2.
 XX
 XX 22-NOV-2001.
 XX
 XX 14-MAY-2001; 2001WO-US15567.
 XX
 XX 12-MAY-2000; 2000US-204039P.
 XX
 XX 27-JUN-2000; 2000US-214591P.
 XX
 XX 14-MAY-2001; 2001US-0214591.
 XX
 XX (AMGE-) AMGEN INC.
 PA
 PI Theill LE, Yu G;
 XX
 XX WPI; 2002-066686/09.
 DR N-PSDB; AAD24708.
 XX
 XX
 PT Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand -
 XX
 XX
 PS Disclosure; Fig 1; 94pp; English.
 XX
 XX The invention relates to a method for inhibiting TAC1 (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
 CC family ligand), having the consensus region of TAC1, BCMA, or the TAC1/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hyperactivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human APRIL G70 protein.
 XX
 XX
 SQ Sequence 248 AA;
 Query Match 60.8%; Score 152; DB 23; Length 248;
 Best Local Similarity 100.0%; Pred. No. 3e-133;
 Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 97 GERSRKRRAVLTOKQKSHVLTVPINATSKDSDVTEVMOPALRRGGLQAGYGV 156
 DB 97 GERSRKRRAVLTOKQKSHVLTVPINATSKDSDVTEVMOPALRRGGLQAGYGV 156
 QY 157 IQDAGVYLLVSQVLFQDVTFTMGQVVSREGQROETLFRCSRMPSPHDPRAVNSCYAGV 216
 DB 157 IQDAGVYLLVSQVLFQDVTFTMGQVVSREGQROETLFRCSRMPSPHDPRAVNSCYAGV 216

DB 157 IQDAGVYLLVSQVLFQDVTFTMGQVVSREGQROETLFRCSRMPSPHDPRAVNSCYAGV 216
 QY 217 FHLHQGDILSVIIPRAKAKNLSPHGTFLGFV 248
 DB 217 FHLHQGDILSVIIPRAKAKNLSPHGTFLGFV 248
 RESULT 29
 AAAM8369
 ID AAAM8369 standard; Protein; 147 AA.
 XX
 AC AAAM8369;
 XX
 XX 26-APR-1999 (first entry)
 DT
 XX
 DE Tumour necrosis factor-gamma soluble polypeptide.
 XX
 XX Tumour necrosis factor-gamma; TNF-gamma; human; inflammation;
 KW cancer; tumour; metastasis; graft versus host disease;
 KW drug screening; therapy; diagnosis.
 XX
 OS Homo sapiens.
 XX
 XX WO9900518-A1.
 PN
 XX 07-JAN-1999.
 PD
 XX
 PF 12-JUN-1998; 98WO-US12101.
 XX
 PR 26-JUN-1997; 97US-0883086.
 XX
 XX (ABBO) ABBOTT LAB.
 PA
 PI Wiley SR;
 XX
 XX WPI; 1999-095761/08.
 DR
 XX
 PT Tumour necrosis factor gamma detects target polynucleotides - useful
 PT for, e.g. treating inflammation, cancer and graft versus host
 PT disease
 XX
 XX
 PS Claim 16; Page 85; 106pp; English.
 XX
 XX This soluble polypeptide comprises amino acid residues 104-250 of
 CC human tumour necrosis factor gamma (TNFG, see AAM8368), a novel
 CC member of the TNF family of ligands. The soluble polypeptide
 CC interacts with the cognate receptor, and induces biological
 CC activity. It can be prepared by recombinant DNA methods, and used
 CC to treat deficiencies of TNFG and disease conditions ameliorated by
 CC TNFG. Antibodies, antagonists and inhibitors of the polypeptide
 CC may be used to treat TNFG-associated diseases, tumours or
 CC metastases, and to screen for, diagnose and monitor conditions
 CC attributable to TNFG, especially inflammation, cancer and graft
 CC versus host disease.
 CC
 XX
 SQ Sequence 147 AA;
 Query Match 58.8%; Score 147; DB 20; Length 147;
 Best Local Similarity 100.0%; Pred. No. 1.4e-134;
 Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 104 RAVLTOKQKSHVLTVPINATSKDSDVTEVMOPALRRGGLQAGYGV 163
 DB 1 RAVLTOKQKSHVLTVPINATSKDSDVTEVMOPALRRGGLQAGYGV 60
 QY 164 LLYSQVLFQDVTFTMGQVVSREGQROETLFRCSRMPSPHDPRAVNSCYAGV 223
 DB 61 LLYSQVLFQDVTFTMGQVVSREGQROETLFRCSRMPSPHDPRAVNSCYAGV 223
 QY 224 ILSVITPRARAKNLSPHGTFLGFV 250
 DB 121 ILSVITPRARAKNLSPHGTFLGFV 147

RESULT 30
AA014134
ID AA014134 standard; Protein: 177 AA.
AC
XX AA014134;
XX
DT 02-MAY-2002 (first entry)
XX
DE Protein of a FLAG tagged human APRIL (soluble).
XX
XX Human transmembrane activator CAML interactor protein; TACI; cytostatic;
KM cell proliferation; tumour; vulvectomy; renal cell cancer; mastocytoma;
KM Kaposi's sarcoma; breast; ovarian carcinoma; rectal; throat; melanoma;
KM colon; bladder; mammary adenocarcinoma; gastrointestinal; hyperplasia;
KM pharyngeal squamous cell; stomach; cellular hyperproliferation; pannus;
KM scleroderma; rheumatoid arthritis; scarring; mean survival time; liver;
KM lung fibrosis; uterine; a proliferation inducing ligand.
XX
XX Homo sapiens.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..15
FT /note= "HA signal sequence tag"
FT Region 16..23
FT /note= "FLAG epitope tag"
FT Region 24..31
FT /note= "Short linker sequence"
FT Region 32..177
FT /note= "Soluble human APRIL sequence"
XX
XX WO200181417-A2.
XX
XX 01-NOV-2001.
XX
XX 27-APR-2001; 2001WO-US40626.
XX
XX 27-APR-2000; 2000US-199946P.
XX
XX (BIOJ) BIOGEN INC.
XX (APOT-) APOTTECH R & D SA.
XX
XX Ambrose C, Thompson J, Schneider P, Rennett P;
XX WPI: 2002-062027/08.
XX N-PSDB; AAK98730.
XX
XX Treating mammal for condition associated with undesired cell
XX proliferation e.g., solid tumour or reducing solid tumour size located in
XX mammal comprises administering transmembrane activator CAML interactor
XX protein reagent -
XX
XX Examples; Fig 9; 42pp; English.
XX
XX This sequence represents the protein of a FLAG tagged human APRIL (A
XX Proliferation inducing ligand) (soluble). The invention relates to
XX treating a mammal for a condition associated with undesired cell
XX proliferation (e.g. a solid tumour, or reducing the size of a solid
XX tumour located on or in a mammal) comprising administering a
XX transmembrane activator CAML interactor protein (TACI) reagent. The TACI
XX reagent has cytostatic and vulvectomy activity. Treating a mammal (e.g.
XX human, cow, horse, dog, mouse, rat or cat) for a condition associated
XX with undesired cell proliferation (e.g. cancer such as renal cell cancer,
XX Kaposi's sarcoma, breast cancer, sarcoma, ovarian carcinoma, rectal
XX cancer, throat cancer, melanoma, colon cancer, bladder cancer,
XX mastocytoma, lung cancer, mammary adenocarcinoma, pharyngeal squamous
XX cell carcinoma, gastrointestinal cancer or stomach cancer). The method is
XX also useful for treating cellular hyperproliferation (hyperplasia) such
XX as scleroderma, pannus formation in rheumatoid arthritis, post-surgical
XX scarring and lung, liver and uterine fibrosis. The TACI reagent of the
XX invention can extend mean survival time of a mammal by 25% as compared to
XX the mean survival time of a mammal in the absence of administering the

CC TACI reagent. The TACI reagent also reduces the size of the tumour by 25%
XX or more.
XX
XX Sequence 177 AA;
SQ
Query Match 58.4%; Score 146; DB 23; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.5e-133;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 105 AVLTQKQKQSHVHLVPINATSKDDSPTEVMQPALRRGRGLQAGYGVRIODAGVYL 164
DB 32 AVLTQKQKQSHVHLVPINATSKDDSPTEVMQPALRRGRGLQAGYGVRIODAGVYL 91
OY 165 LYSQVLFQDVTFTMGQVVSREGQROETLFRICISMPSPHPRAYNSCYSAGVFHLQCDI 224
DB 92 LYSQVLFQDVTFTMGQVVSREGQROETLFRICISMPSPHPRAYNSCYSAGVFHLQCDI 151
OY 225 LSVIIPRARAKLNSPHTGTFGLFVKL 250
DB 152 LSVIIPRARAKLNSPHTGTFGLFVKL 177
RESULT 31
AAE00505
ID AAE00505 standard; Protein: 172 AA.
XX
XX AAE00505;
XX
XX 31-JUL-2001 (first entry)
XX
XX FLAG-human A Proliferation Inducing Ligand (APRIL) protein construct.
XX
XX Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
XX gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
XX carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
XX systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
XX B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
XX organ transplantation; HIV; human immunodeficiency virus; TNF;
XX tumour necrosis factor; B cell maturation protein; BCMA; FLAG epitope.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 1..15
XX /label= "Signal_peptide"
XX Protein 16..172
XX /label= Mature_FLAG-human_A_Proliferation_inducing_Ligand
XX FT protein_construct
XX FT 16..23
XX /label= FLAG_epitope
XX
XX WO200124811-A1.
XX
XX 12-APR-2001.
XX
XX 05-OCT-2000; 2000WO-US27579.
XX
XX 06-OCT-1999; 99US-0157933.
XX 11-FEB-2000; 2000US-0181807.
XX 30-JUN-2000; 2000US-0215688.
XX
XX (BIOJ) BIOGEN INC.
XX (APOT-) APOTTECH R & D SA.
XX
XX Schneider P, Thompson J, Cachero T, Ambrose C, Rennett P;
XX WPI: 2001-266242/27.
XX N-PSDB; AAD03842.
XX
XX Treating a mammal for a condition associated with undesired cell
XX proliferation such as cancer or carcinoma, comprises administering a
XX composition comprising A Proliferation Inducing Ligand Receptor

PT (APRIL-R) antagonist -
 XX Example 2; Fig 2; 85pp; English.
 PS
 CC The invention relates to a method of treating a mammal for a condition
 CC associated with undesired cell proliferation such as cancer or
 CC carcinoma. The method involves administering a composition comprising
 CC A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as
 CC B cell maturation protein (BCM or BCMa) antagonist that antagonises the
 CC interaction between APRIL and its cognate receptor(s). This method is
 CC useful for treating undesired cell proliferation such as cancer or
 CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
 CC prostate carcinoma, and other carcinomas whose proliferation is modulated
 CC by APRIL. It is also useful for treating autoimmune diseases (Grave's
 CC disease, systemic lupus erythematosus-SLE), hypertension, cardiovascular
 CC diseases, renal disorders, B-cell lympho-proliferative disorders,
 CC immunosuppressive diseases, organ transplantation, inflammation and
 CC human immunodeficiency virus (HIV), and for treating, suppressing or
 CC altering an immune response involving a signalling pathway between
 CC APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy.
 CC The present sequence is FLAG-human A Proliferation Inducing Ligand
 CC (APRIL) protein construct. This sequence comprises FLAG epitope,
 CC followed by human APRIL extracellular domain. APRIL is a member of
 CC Tumour Necrosis Factor (TNF) family of proteins.
 CC
 XX Sequence 172 AA;
 SQ
 Query Match 56.8%; Score 142; DB 22; Length 172;
 Best Local Similarity 100.0%; Pred. No. 1.1e-129; Indels 0; Gaps 0;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 109 QOKQKHSHVHLVPIINATSKDSDVTEVMQPALRRGRGLQAOGYGVRIODAGVYLLYSQ 168
 DB 31 QOKQKHSHVHLVPIINATSKDSDVTEVMQPALRRGRGLQAOGYGVRIODAGVYLLYSQ 90
 QY 169 VLFQDVFTMGQVVSREGQROETLFRICRSMPSHPDAVNSCSAGVFHLHOGDILSVI 228
 DB 91 VLFQDVFTMGQVVSREGQROETLFRICRSMPSHPDAVNSCSAGVFHLHOGDILSVI 150
 QY 229 IPRARAKLNLSPHGTFLGFKVL 250
 DB 151 IPRARAKLNLSPHGTFLGFKVL 172

RESULT 32
 AAW37002
 ID AAW37002 standard; Protein: 233 AA.
 AAW37002;
 DT 14-APR-1998 (first entry)
 XX
 DE Human tumour necrosis factor delta.
 XX
 KW Human; tumour necrosis factor delta; TNF-delta; TNF-epsilon; cancer;
 KW tumour necrosis factor epsilon; T cell proliferation;
 KW immune regulation; inflammatory response.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT MISC-difference 231..233
 FT /note= "Not given in the specification but present
 FT if the CDNA is fully decoded"

XX
 PN W09733902-A1.
 XX
 PD 18-SEP-1997.
 XX
 PF 14-MAR-1996; 96WO-US03774.
 XX
 PR 14-MAR-1996; 96WO-US03774.
 XX

PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Gentz RL, Ni J, Yu G;
 XX
 DR WPI: 1997-470810/43.
 DR N-PSDB; AAV00493.
 PS
 XX Claim 18; Fig 1; 83pp; English.
 CC
 CC The present sequence represents human tumour necrosis factor (TNF)
 CC delta. The TNF can be used to treat patients deficient in this factor
 CC (optionally by in vivo expression). It is a ligand for TNF and can
 CC destroy (by inducing apoptosis) some transformed cell lines (for tumour
 CC treatment); mediate cell activity and proliferation (including T cells
 CC to stimulate an immune response to viral, bacterial or parasitic
 CC infections), also to eliminate autoreactive T cells in e.g. type 1
 CC (diabetes), and is functionally linked as a primary mediator of immune
 CC regulation and the inflammatory response. A typical application of the
 CC protein, its agonists or antagonists is prevention of septic shock,
 CC inflammation, cerebral malaria, human immunodeficiency virus activation,
 CC graft-host reaction, bone resorption (osteoporosis), rheumatoid
 CC arthritis and cachexia, also to promote wound healing (by upregulating
 CC cell adhesion) and to regulate haematopoiesis. The protein can also be
 CC used to isolate its cognate receptors (or receptor-encoding genes).
 CC The CDNA can be used to produce recombinant proteins, and fragments of
 CC it to isolate full-length or related sequences, for diagnostic detection
 CC of mutations (indicative of disease or susceptibility) and for
 CC chromosome identification. Analysis of patient samples for presence of
 CC the new protein (e.g. using specific antibodies) can be used
 CC diagnostically.
 CC
 XX Sequence 233 AA;
 SQ
 Query Match 56.8%; Score 142; DB 18; Length 233;
 Best Local Similarity 100.0%; Pred. No. 1.5e-129;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 109 QOKQKHSHVHLVPIINATSKDSDVTEVMQPALRRGRGLQAOGYGVRIODAGVYLLYSQ 168
 DB 92 QOKQKHSHVHLVPIINATSKDSDVTEVMQPALRRGRGLQAOGYGVRIODAGVYLLYSQ 151
 QY 169 VLFQDVFTMGQVVSREGQROETLFRICRSMPSHPDAVNSCSAGVFHLHOGDILSVI 228
 DB 152 VLFQDVFTMGQVVSREGQROETLFRICRSMPSHPDAVNSCSAGVFHLHOGDILSVI 211
 QY 229 IPRARAKLNLSPHGTFLGFKVL 250
 DB 212 IPRARAKLNLSPHGTFLGFKVL 233

RESULT 33
 AAB08661
 ID AAB08661 standard; Protein: 136 AA.
 AAB08661;
 AC
 XX
 DT 02-JAN-2001 (first entry)
 XX
 DE A fragment of human neutrophilic alpha polypeptide.
 XX
 KW Human; neutrophilic alpha; tumor metastasis; infection;
 KW immunodeficiency; inflammatory disease; lymphadenopathy; dermatitis;
 KW autoimmune disease; graft versus host disease; immune regulation;
 KW severe combined immunodeficiency-X-linked agammaglobulinemia;
 KW kappa chain deficiency; B cell lymphoproliferative disorder; purpura;
 KW Wiskott-Aldrich syndrome; systemic lupus erythematosus; myocarditis;
 KW idiopathic thrombocytopenia purpura; hemolytic anemia; neuritis;
 KW allergic encephalomyelitis; relapsing polychondritis; glomerulonephritis;
 KW rheumatic heart disease; multiple sclerosis; uveitis; ophtalmia;
 KW

XX The present invention relates to a new antibody, or portion, that
 CC specifically binds to a protein which has a 285 or 250 amino acid
 CC sequence as fully defined in the specification. The antibody of the
 CC invention is useful in treating a disease or disorder such as cancer,
 CC especially B-cell cancer, autoimmune diseases such as Sjogren's
 CC syndrome, systemic lupus erythematosus, rheumatoid arthritis, chronic
 CC lymphocytic leukaemia, multiple myeloma, Hodgkin's lymphoma,
 CC non-Hodgkin's lymphoma or hypergammaglobulinemia, or in diagnosing a
 CC disease or disorder comprising assaying expression of Neutrokin- α
 CC and APRIL (a proliferation-inducing ligand) in cells or body fluids using
 CC antibodies and comparing the Neutrokin- α and APRIL expression level
 CC with a standard Neutrokin- α and APRIL expression level, whereby an
 CC increase or decrease in the assayed Neutrokin- α and APRIL expression
 CC level compared to the standard levels is indicative of a disease or
 CC disorder. The present amino acid sequence represents the human APRIL
 CC protein #1 of the invention.

Sequence 136 AA:
 SQ
 Query Match 54.4%; Score 136; DB 23; Length 136;
 Best Local Similarity 100.0%; Pred. No. 6.2e-124; Mismatches 0; Gaps 0;
 Matches 136; Conservative 0; Indels 0; Gaps 0;

QY 115 HSVLHLVINTSKDSDVTEVMQPALRRGRGLAQGYGVRIODAGVYLVSQVLFQDV 174
 DB 1 HSVLHLVINTSKDSDVTEVMQPALRRGRGLAQGYGVRIODAGVYLVSQVLFQDV 60

QY 175 TFTMGQVVSRRSGQROETLFCIRSMPSHPRAVNSCAGVFHLHOGDILSVIIPARA 234
 DB 61 TFTMGQVVSRRSGQROETLFCIRSMPSHPRAVNSCAGVFHLHOGDILSVIIPARA 120

QY 235 KLNLSPHGTFILGFVKL 250
 DB 121 KLNLSPHGTFILGFVKL 136

RESULT 35
 AAE07877
 ID AAE07877 standard; Protein: 248 AA.

AC AAE07877;
 XX
 DT 01-NOV-2001 (first entry)
 XX
 DE Human APRIL protein.
 XX
 KM Human; tumour necrosis factor; TNF; APBF; APRIL; BAF; therapy; melanoma;
 KM immune system-related disorder; cancer; renal cell; breast; stomach;
 KM rectal; colon; throat; bladder; ovarian carcinoma; cellular disorder;
 KM gastrointestinal; scleroderma; Kaposi's sarcoma; chronic leukaemia;
 KM squamous cell carcinoma; hyperproliferative condition; pannus formation;
 KM rheumatoid arthritis; postsurgical scarring; fibrosis; liver; uterine;
 KM lung; immunodeficiency; inflammatory disease; lymphadenopathy; vulvetry;
 KM autoimmune disease; graft versus host disease; dermatological;
 KM antiinflammatory; immunosuppressive; cytostatic.

OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 16
 FT Region /note= "Encoded by GGC"
 FT /label= Transmembrane_region
 FT Misc-difference 32..33
 FT /note= "Encoded by TGTTGAGT"
 FT Misc-difference 43
 FT /note= "Encoded by TGT"
 FT Misc-difference 70..72
 FT /note= "Encoded by CCTCCAG"
 FT Misc-difference 102..104
 FT /note= "Encoded by AGGAGCA"
 FT Region 108..117

FT /note= "N-terminal of the recombinant soluble APRIL
 FT sequence"
 FT Modified-site 123
 FT /note= "N-glycosylated"
 FT Misc-difference 174
 FT /note= "Encoded by ACT"
 FT Misc-difference 176
 FT /note= "Encoded by ACC"
 FT Misc-difference 220..221
 FT /note= "Encoded by CAAGGAGT"
 XX
 PN W0200158949-A2.
 XX
 XX 16-AUG-2001.
 PD
 XX
 PF 08-FEB-2001: 2001WO-US04121.
 XX
 PR 11-FEB-2000: 2000US-0181670.
 XX
 PA (BIOJ) BIOGEN INC.
 PI Renner PD, Thompson JS, Ambrose C, Cachero TG;
 DR WPI: 2001-514644/56.
 DR N-PSDB: AAD14415.
 XX
 PS Claim 2; Fig 1a; 42pp; English.

CC The present invention relates to an isolated heteromeric ligand of
 CC tumour necrosis factor (TNF)-family, referred to as APBF comprising a
 CC TNF-family member APRIL subunit linked non-covalently to TNF-family
 CC member BAF subunit. APBF is useful for diagnosis or treatment of
 CC various immune system-related disorders in mammals, preferably humans.
 CC Such disorders include cancer, including cellular disorders, for e.g.
 CC renal cell cancer, Kaposi's sarcoma, chronic leukaemia, breast cancer,
 CC sarcoma, ovarian carcinoma, rectal cancer, throat cancer, melanoma,
 CC colon cancer, bladder cancer, squamous cell carcinoma and
 CC gastrointestinal or stomach cancer, cellular hyperproliferative
 CC conditions, such as scleroderma, pannus formation in rheumatoid
 CC arthritis, postsurgical scarring and lung, liver and uterine fibrosis
 CC and immunodeficiencies, inflammatory diseases, lymphadenopathy,
 CC autoimmune diseases and graft versus host disease. APBF is also useful
 CC for producing monoclonal or polyclonal antibodies and for identifying
 CC novel modulators affecting biological function and receptors interacting
 CC with APBF. The present sequence is human APRIL protein.

SO Sequence 248 AA;
 Query Match 52.0%; Score 130; DB 22; Length 248;
 Best Local Similarity 100.0%; Pred. No. 7.1e-118;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 AMALLTQOTELQSLRRVSLRGCTGSPGNGEGYPMQSLPEQSSDALEAENGSRKKR 104
 DB 44 AMALLTQOTELQSLRRVSLRGCTGSPGNGEGYPMQSLPEQSSDALEAENGSRKKR 103

QY 105 AVLTKQKQKSHVLAIVINATSKDSDVTEVMQPALRRGRGLAQGYGVRIODAGVYL 164
 DB 104 AVLTKQKQKSHVLAIVINATSKDSDVTEVMQPALRRGRGLAQGYGVRIODAGVYL 163

QY 165 LYSQVLFQDV 174
 DB 164 LYSQVLFQDV 173

RESULT 36
 AAB64873
 ID AAB64873 standard; Protein: 123 AA.

XX AAB64873;
AC
XX
XX 23-MAR-2001 (first entry)
DE
XX
XX Gene 44 human secreted protein homologous amino acid sequence #159.
XX
XX Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;
KM antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KM neurotropic; neuroprotective; antibacterial; virucide; fungicide;
KM ophthalmological; autoimmune disease; hyperproliferative disorder;
KM cardiovascular disorder; cerebrovascular disorder; infection; chemotaxis;
KM nervous system disorder; ocular disorder; skin aging; wound healing;
KM food additive; tissue regeneration.
XX
XX Homo sapiens.
OS
XX WO200077256-A1.
PN
XX 21-DEC-2000.
XX
XX 01-JUN-2000; 2000WO-US14963.
DE
XX 11-JUN-1999; 99US-0138631.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Rosen CA, Ruben SM, Komatsoulis GA;
PI
XX WPI; 2001-032315/04.
DR
XX
XX Isolated nucleic acid molecule encoding a human secreted protein is
PT used in preventing, treating or ameliorating a medical condition -
XX
XX Disclosure: Page 86; 506pp; English.
PS
XX
XX Polynucleotide sequences AAF33095 - AAF33142 encode human secreted
CC proteins AAB64773 - AAB64820. Fragments of the secreted proteins and
CC amino acid sequences which share homology with the fragments are
CC represented in AAB64821 - AAB64880. The genes and proteins have
CC activities dependent on the tissues and cells in which they are
CC expressed. Examples of their activities and the activities of their
CC agonists and antagonists include; immunosuppressive; antiarthritic;
CC antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
CC cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide;
CC fungicide; and ophthalmological. The secreted proteins, polynucleotides,
CC antagonists and agonists may be useful in treating, preventing and
CC diagnosing diseases and disorders such as autoimmune diseases e.g.
CC rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the
CC breast or liver, cardiovascular disorders e.g. cardiac arrest,
CC cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous
CC system disorders e.g. Alzheimer's disease, infections caused by bacteria,
CC viruses and fungi and ocular disorders e.g. corneal infection. The
CC polypeptides can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues and in chemotaxis. The polypeptides can also be
CC used as a food additive or preservative to increase or decrease storage
CC capabilities. Included in the invention are sequences AAB64772 and
CC AAF33095 - AAF33142 which are used in the isolation and characterisation
CC of the nucleotide and protein sequences of the invention.
XX
XX Sequence 123 AA;
SQ

Query Match 49.2%; Score 123; DB 22; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.4e-111;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 KDDSDVTEVMWOPALRRGRLGLOAGVSRITDAGVYLLYSOVLFOVPTMTMGVVSREGQ 187
DB 1 KDDSDVTEVMWOPALRRGRLGLOAGVSRITDAGVYLLYSOVLFOVPTMTMGVVSREGQ 60
QY 188 GROETLFRICIRSMPSHPBRAVNSCVSAGVFLHQGDILSVIIPARAKLNLSPHGTGLGF 247

DB 61 GROETLFRICIRSMPSHPBRAVNSCVSAGVFLHQGDILSVIIPARAKLNLSPHGTGLGF 120
QY 248 VKL 250
DB 121 VKL 123

RESULT 37
AAM37003
ID AAM37003 standard; Protein: 168 AA.
XX
XX AAM37003;
AC
XX
XX 14-APR-1998 (first entry)
DE
XX Human tumour necrosis factor epsilon.
XX
XX Human; tumour necrosis factor delta; TNF-delta; TNF-epsilon; cancer;
KM tumour necrosis factor epsilon; T cell proliferation;
KM immune regulation; inflammatory response.
XX
XX Homo sapiens.
OS
XX WO9733902-A1.
PN
XX 18-SEP-1997.
XX
XX 14-MAR-1996; 96WO-US03774.
DE
XX 14-MAR-1996; 96WO-US03774.
XX
XX 14-MAR-1996; 96WO-US03774.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Gentz RL, Ni J, Yu G;
PI
XX WPI; 1997-470810/43.
DR
XX N-PSDB; AAV00494.
XX
XX Nucleic acid encoding human tumour necrosis factors delta and
PT epsilon - useful for destroying cancer cells, or mediating T cell
PT proliferation, immune regulation and inflammatory responses etc.
XX
XX Claim 20; Fig 2; 83pp; English.
XX
XX The present sequence represents human tumour necrosis factor (TNF)
CC epsilon. The TNF can be used to treat patients deficient in this factor
CC (optionally by in vivo expression). It is a ligand for TNF and can
CC destroy (by inducing apoptosis) some transformed cell lines (for tumour
CC treatment); mediate cell activity and proliferation (including T cells
CC to stimulate an immune response to viral, bacterial or parasitic
CC infections, also to eliminate autoreactive T cells in e.g. type I
CC diabetes), and is functionally linked as a primary mediator of immune
CC regulation and the inflammatory response. A typical application of the
CC protein, its agonists or antagonists is prevention of septic shock,
CC inflammation, cerebral malaria, human immunodeficiency virus activation,
CC graft-host reaction, bone resorption (osteoporosis), rheumatoid
CC arthritis and cachexia, also to promote wound healing (by upregulating
CC cell adhesion) and to regulate haematopoiesis. The protein can also be
CC used to isolate its cognate receptors (or receptor-encoding genes).
CC The cDNA can be used to produce recombinant proteins, and fragments of
CC it to isolate full-length or related sequences, for diagnostic detection
CC of mutations (indicative of disease or susceptibility) and for
CC chromosome identification. Analysis of patient samples for presence of
CC the new protein (e.g. using specific antibodies) can be used
CC diagnostically.
XX
XX Sequence 168 AA;
SQ

Query Match 48.4%; Score 121; DB 18; Length 168;
Best Local Similarity 100.0%; Pred. No. 2.8e-109;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 DSDVTEVMQPALRGRLQAGYGVRIQDAGVYLVSQVLFQDVTFTMGQVSRREGGR 189
 DB 48 DSDVTEVMQPALRGRLQAGYGVRIQDAGVYLVSQVLFQDVTFTMGQVSRREGGR 107
 QY 190 QETLFCIRSMPSHPDRAYNSCYSAGVFHLHOGDILSVIIPRAKXNLSPHGFLGFVK 249
 DB 108 QETLFCIRSMPSHPDRAYNSCYSAGVFHLHOGDILSVIIPRAKXNLSPHGFLGFVK 167
 QY 250 L 250
 DB 168 L 168

RESULT 38
 AAU95509
 ID AAU95509 standard; Protein, 168 AA.

AC AAU95509;
 XX 07-OCT-2002 (first entry)

Human tumour necrosis factor (TNF) epsilon #1.

Human, tumour necrosis factor; TNF epsilon; pulmonary system disorder; immunoglobulin production; B-cell proliferation; immune system disorder; autoimmune disease; cancer; lymphoproliferative disorder; pain; microbial infection; parasitic infection; bone disease; atherosclerosis; cardiovascular disorder; neurodegenerative disease; wound healing; graft versus host disease; haematopoietic cell disorder; nephritis; inflammatory disorder; mucous membrane disorder; dermatological; immunosuppressive; cytostatic.

Homo sapiens.
 OS
 PN US2002064829-A1.
 PD 30-MAY-2002.
 XX 14-JUN-2001; 2001US-0879919.
 PF 14-MAR-1996; 96US-016812P.
 PR 15-JUN-2000; 2000US-211537P.
 PR 23-OCT-2000; 2000US-241952P.
 PR 13-DEC-2000; 2000US-254875P.
 PR 16-MAR-2001; 2001US-276248P.
 PR 23-MAR-2001; 2001US-277978P.
 PR 25-MAY-2001; 2001US-293499P.
 PR 12-MAR-1997; 97US-0815783.

(HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Yu G, N1 J, Gentz RL, Dillon PJ;
 DR WPI; 2002-556722/59.
 DR N-PSDB; ABB88684.
 XX
 PT Novel human multimeric tumour necrosis factor delta or epsilon protein
 PT useful for treating disease or disorder of immune system such as
 PT autoimmune disease, immunodeficiency, or cancer of immune system -
 PT
 Claim 1; Fig 2; 143p; English.

The present invention relates to the isolation of human tumour necrosis factor (TNF) delta and TNF epsilon proteins, and the polynucleotide sequences encoding them. The proteins are useful for modulating immunoglobulin production or for modulating proliferation of B-cells. The sequences of the invention are useful for treating diseases or disorders of the immune system. Such disorders include autoimmune diseases (e.g. systemic lupus erythematosus (SLE), acquired immunodeficiency syndrome (AIDS)), cancers of the immune system (e.g. chronic lymphocytic leukaemia (CLL), multiple myeloma, non-Hodgkin's lymphoma or Hodgkin's disease), lymphoproliferative disorders, microbial infections (e.g. viral, bacterial), parasitic

CC infections, nephritis, bone disease (e.g. osteoporosis), atherosclerosis,
 CC pain, cardiovascular disorders (e.g. myocardial infarction, stroke),
 CC neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's
 CC disease), graft versus host disease, wound healing, haematopoietic cell
 CC disorders (e.g. anemia), inflammatory disorders (e.g. asthma),
 CC diseases or disorders associated with various mucous membranes of the
 CC body (e.g. mucositis), and disorders of the pulmonary system. The
 CC proteins are also useful as a vaccine adjuvant that enhances immune
 CC responsiveness to specific antigens. The present sequence represents
 CC human TNF epsilon #1.
 XX

Sequence 168 AA;
 SQ

Query Match 48.4%; Score 121; DB 23; Length 168;
 Best Local Similarity 100.0%; Pred. No. 2.8e-109;
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 DSDVTEVMQPALRGRLQAGYGVRIQDAGVYLVSQVLFQDVTFTMGQVSRREGGR 189
 DB 48 DSDVTEVMQPALRGRLQAGYGVRIQDAGVYLVSQVLFQDVTFTMGQVSRREGGR 107
 QY 190 QETLFCIRSMPSHPDRAYNSCYSAGVFHLHOGDILSVIIPRAKXNLSPHGFLGFVK 249
 DB 108 QETLFCIRSMPSHPDRAYNSCYSAGVFHLHOGDILSVIIPRAKXNLSPHGFLGFVK 167
 QY 250 L 250
 DB 168 L 168

RESULT 39
 AAU75403
 ID AAU75403 standard; Protein, 168 AA.

AC AAU75403;
 XX 09-APR-2002 (first entry)

Tumour necrosis factor epsilon (TNF-epsilon), variant #1.

Tumour necrosis factor epsilon; TNF-epsilon; cytostatic; atherosclerosis; analgesic; cerebroprotective; neurotropic; neuroprotective; hepatotropic; immunoglobulin production; B cell proliferation; immunosuppressive; autoimmune disease; HIV; human immunodeficiency virus; immunodeficiency; Sjogren's syndrome; systemic lupus erythematosus; Hodgkin's disease; common variable immunodeficiency; CVID; non-Hodgkin's lymphoma; AIDS; acquired immunodeficiency virus; cancer; multiple myeloma; CLL; chronic lymphocytic leukaemia; lymphoproliferative disorder; bacterial infection; viral infection; osteoporosis; atherosclerosis; pain; cardiovascular disorder; stroke; allergy; Alzheimer's disease; neurodegenerative disease; inflammation; liver disease; cirrhosis; cardiomyopathy; diabetes; asthma; psoriasis; glomerulonephritis; ulcerative colitis; angiogenesis; septic shock; wound healing.

Homo sapiens.
 OS
 XX
 FH Key location/Qualifiers
 FT Peptide 1..38
 FT /label= Signal_peptide
 FT Protein 39..168
 FT /label= Mature_TNF-epsilon
 FT /note= "Mature TNF-epsilon factor, specifically claimed in claim 1"
 FT
 FT Domain 10..17
 FT /label= Conserved_domain_1
 FT /note= "Region of high identity between TNF-delta
 FT and TNF-epsilon"
 FT
 FT Domain 47..56
 FT /label= Conserved_domain_III
 FT /note= "Region of high identity between TNF-delta
 FT and TNF-epsilon"
 FT
 FT Domain 61..74

FT /label= Conserved domain IV
 FT /note= "Region of high identity between TNF-delta
 FT and TNF-epsilon"
 FT 73..89
 FT /note= "TNF family signature sequence"
 FT 79..89
 FT /label= Conserved domain V
 FT /note= "Region of high identity between TNF-delta
 FT and TNF-epsilon"
 FT 101..111
 FT /label= Conserved domain VI
 FT /note= "Region of high identity between TNF-delta
 FT and TNF-epsilon"
 FT 114..119
 FT /label= Conserved domain VII
 FT /note= "Region of high identity between TNF-delta
 FT and TNF-epsilon"
 FT 126..130
 FT /label= Conserved domain VIII
 FT /note= "Region of high identity between TNF-delta
 FT and TNF-epsilon"
 FT 133..144
 FT /label= Conserved domain IX
 FT /note= "Region of high identity between TNF-delta
 FT and TNF-epsilon"
 FT 147..154
 FT /label= Conserved domain X
 FT /note= "Region of high identity between TNF-delta
 FT and TNF-epsilon"
 FT 164..168
 FT /label= Conserved domain XI
 FT /note= "Region of high identity between TNF-delta
 FT and TNF-epsilon"
 FT Domain
 FT WO200196528-A2.
 FT 20-DEC-2001.
 FT 14-JUN-2001; 2001WO-US19026.
 FT 15-JUN-2000; 2000US-211537P.
 FT 23-OCT-2000; 2000US-241952P.
 FT 13-DEC-2000; 2000US-254875P.
 FT 16-MAR-2001; 2001US-276248P.
 FT 23-MAR-2001; 2001US-277978P.
 FT 25-MAY-2001; 2001US-293499P.
 FT (HUMA-) HUMAN GENOME SCI INC.
 FT Yu G, Ni J, Gentz RL, Dillon PJ, Hilbert D;
 FT WPI, 2002-130727/17.
 FT N-PSDB; ABK13402.
 FT Novel multimeric human tumour necrosis factor delta or epsilon protein
 FT useful for treating cancer, immune system disorders, infection,
 FT cardiovascular disorders, liver disease, cardiomyopathy, diabetes and
 FT psoriasis -
 FT Claim 1; Fig 2A; 344p; English.
 PS The invention describes a multimeric human tumour necrosis factor (TNF)
 CC delta or epsilon protein (I). (I) or a composition containing them (II)
 CC are useful for modulating immunoglobulin production or proliferation of B
 CC cells. (I) or (II) is useful for treating a disease or disorder of the
 CC immune system, preferably an autoimmune disease (e.g. Sjogren's syndrome,
 CC systemic lupus erythematosus or common variable immunodeficiency (CVID));
 CC an immunodeficiency e.g. acquired immunodeficiency syndrome (AIDS);
 CC cancer of the immune system (e.g. Hodgkin's disease, non-Hodgkin's
 CC lymphoma, multiple myeloma and chronic lymphocytic leukaemia (CLL)); in
 CC the diagnosis and treatment or prevention of cancer, lymphoproliferative
 CC disorder, bacterial and viral infections, osteoporosis, atherosclerosis,
 CC pain, cardiovascular disorders (e.g. stroke), allergy, inflammation,

CC neurodegenerative disease (e.g. Alzheimer's disease), liver disease (e.g.
 CC cirrhosis), cardiomyopathy, diabetes, asthma, psoriasis, septic shock,
 CC glomerulonephritis, ulcerative colitis, arteriosclerosis; for promoting
 CC angiogenesis and wound healing; as a diagnostic research reagent; as an
 CC agent to target and kill cells expressing a TNFdelta and/or TNFepsilon
 CC receptor; in apoptosis of transformed cell lines; mediation of cell (II)
 CC activation and proliferation; and as an immunogen to produce (II). (II)
 CC is useful to purify, detect and target (I), for measuring levels of (I)
 CC in biological samples, for immunophenotyping samples, and to treat,
 CC inhibit or prevent diseases and disorders associated with aberrant
 CC expression and/or activity of (I). This is the amino acid sequence of
 CC human tumour necrosis factor epsilon (TNF-epsilon) variant #1,
 CC described in the method of the invention.
 CC
 SQ Sequence 168 AA;
 Query Match 48.4%; Score 121; DB 23; Length 168;
 Best Local Similarity 100.0%; Pred. No. 2.8e-109; Indels 0; Gaps 0;
 Matches 121; Conservative 0; Mismatches 0;
 Oy 130 DSDYTEVMMQPALRRGGLQAGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREGGR 189
 Db 48 DSDYTEVMMQPALRRGGLQAGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREGGR 107
 Oy 190 QETLFRICIRSMPSHPDRAYNSCYAGVFHLLHQGDILSVIIPRAKLNLSPHGTFLGFKV 249
 Db 108 QETLFRICIRSMPSHPDRAYNSCYAGVFHLLHQGDILSVIIPRAKLNLSPHGTFLGFKV 167
 Oy 250 L 250
 Db 168 L 168
 RESULT 40
 AAY28835
 ID AAY28835 standard; Protein: 234 AA.
 AC AAY28835;
 XX
 DT 17-JAN-2000 (first entry)
 XX
 DE Human TNF-related death ligand-11.
 XX
 KW Tumour necrosis factor-related death ligand-11; TRDU-11; cytokine;
 KW TNF alpha; Fas ligand; FasL; TNF-related apoptosis-inducing ligand;
 KW TRAIL; cellular apoptosis; transcription factor; NF kappa B; cancer;
 KW autoimmune disease; viral infection; antagonist; AIDS; probe; primer;
 KW neurodegenerative disease; myelodysplastic disease; ischaemic injury;
 KW chromosome localisation; antibody.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT 1..23 Location/Qualifiers
 FT /label= N-terminal_cytoplasmic_domain
 FT 24..52
 FT /label= Transmembrane_domain
 FT 53..234
 FT /label= C-terminal_extracellular_domain
 XX
 PN WO9950416-A1.
 XX
 PD 07-OCT-1999.
 XX
 PF 21-SEP-1998; 98WO-US18506.
 XX
 PR 30-SEP-1997; 97US-0060475.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Bienkowski MJ, Jones DA, Mills CJ;
 XX WPI, 1999-610854/52.

DR N-PSDB; AAX90910.
 XX New nucleic acid used for promotion or inhibition of apoptosis, e.g.
 PT for treating cancer -
 XX
 PS Claim 1; Fig 3; 70pp; English.
 XX
 CC The present sequence is tumour necrosis factor (TNF)-related death
 CC ligand-11 (TRDL-11), that belongs to the C-terminal domain of TNF alpha, Fas
 CC and 12* sequence homology to the C-terminal domains of TNF alpha, Fas
 CC ligand (FasL) and TNF-related apoptosis-inducing ligand (TRAIL)
 CC respectively. It can activate cellular apoptosis-inducing ligand (TRAIL)
 CC NF kappa B and can be used for treating conditions associated with
 CC inadequate levels of apoptosis, like cancer, autoimmune disease and viral
 CC infections. TRDL antagonist can be used to reduce apoptosis levels in
 CC conditions like, AIDS, neurodegenerative diseases, myelodysplastic
 CC disease and ischaemic injury. TRDL gene can be used for chromosome
 CC localisation and as probe or primer for detecting TRDL nucleic acid or
 CC cells that express TRDL. Antibodies generated against TRDL are useful for
 CC detecting TRDL expression.

Sequence 234 AA;

Query Match 48.4%; Score 121; DB 20; Length 234;

Best Local Similarity 100.0%; Pred. No. 3.7e-109;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 DSDVTEVMQPALRRGGLQAGYGVRIQDAGVLLYSQVLFQDVTFTMGQVSRREGGR 189
 |||||
 DB 114 DSDVTEVMQPALRRGGLQAGYGVRIQDAGVLLYSQVLFQDVTFTMGQVSRREGGR 173
 |||||
 QY 190 QETLFCIRSMPSHPDRAYNSCYSAGVFHLHOGDILSVIIPRAKLNLSPHGTFLGFEVK 249
 |||||
 DB 174 QETLFCIRSMPSHPDRAYNSCYSAGVFHLHOGDILSVIIPRAKLNLSPHGTFLGFEVK 233
 |||||
 QY 250 L 250
 |||||
 DB 234 L 234

RESULT 41

AAB62330

ID AAB62330 standard; protein; 234 AA.

XX AAB62330;

AC AAB62330;

XX AAB62330;

DT 29-JUN-2001 (first entry)

XX Human TRDL-1beta polypeptide.

KM Tumour necrosis factor related death ligand-1gamma; TRDL-1gamma; TRDL,
 KM cell death; apoptosis; human; TRDL-1beta.

XX Homo sapiens.

XX WO200125256-A2.

XX 12-APR-2001.

XX 06-OCT-2000; 2000WO-US27868.

XX 06-OCT-1999; 99US-0157913.

XX (UTAH) UNIV UTAH RES FOUND.

XX Jones D, Manos E;

XX WPI; 2001-281728/29.

PT Isolated and purified polynucleotide encoding human tumor necrosis
 PT factor related death ligand (TRDL)-1 gamma useful for identifying
 PT agents that inhibit or enhance TRDL-1 gamma mediated induction of
 PT apoptosis -

XX Disclosure; Fig 1; 39pp; English.
 PS
 XX
 CC The invention provides a human tumour necrosis factor related death
 CC ligand-1gamma (TRDL-1gamma). The TRDL-1gamma polypeptide can be
 CC expressed by standard recombinant methodology. TRDL-1gamma stimulates
 CC Utrka cell death. It is useful for identifying agents capable of
 CC inhibiting or enhancing TRDL-1gamma mediated induction of apoptosis.
 CC The present sequence represents a TRDL-1beta polypeptide, used in
 CC alignment studies.

SQ Sequence 234 AA;

Query Match 48.4%; Score 121; DB 22; Length 234;

Best Local Similarity 100.0%; Pred. No. 3.7e-109;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 DSDVTEVMQPALRRGGLQAGYGVRIQDAGVLLYSQVLFQDVTFTMGQVSRREGGR 189
 |||||
 DB 114 DSDVTEVMQPALRRGGLQAGYGVRIQDAGVLLYSQVLFQDVTFTMGQVSRREGGR 173
 |||||
 QY 190 QETLFCIRSMPSHPDRAYNSCYSAGVFHLHOGDILSVIIPRAKLNLSPHGTFLGFEVK 249
 |||||
 DB 174 QETLFCIRSMPSHPDRAYNSCYSAGVFHLHOGDILSVIIPRAKLNLSPHGTFLGFEVK 233
 |||||
 QY 250 L 250
 |||||
 DB 234 L 234

RESULT 42

AAU99511

ID AAU99511 standard; Protein; 234 AA.

XX AAU99511;

AC AAU99511;

XX AAU99511;

DT 07-OCT-2002 (first entry)

XX Human tumour necrosis factor (TNF) epsilon #2.

KM Human; tumour necrosis factor; TNF epsilon; pulmonary system disorder;
 KM immunoglobulin production; B-cell proliferation; immune system disorder;
 KM autoimmune disease; cancer; lymphoproliferative disorder; pain;
 KM microbial infection; parasitic infection; bone disease; atherosclerosis;
 KM cardiovascular disorder; neurodegenerative disease; wound healing;
 KM graft versus host disease; haematopoietic cell disorder; nephritis;
 KM inflammatory disorder; mucous membrane disorder; dermatological;
 KM immunosuppressive; cytostatic.

XX Homo sapiens.

XX US2002064829-A1.

XX 30-MAY-2002.

XX 14-JUN-2001; 2001US-0879919.

XX 14-MAR-1996; 96US-016812P.

XX 23-OCT-2000; 2000US-211537P.

XX 13-DEC-2000; 2000US-241952P.

XX 16-MAR-2001; 2001US-276248P.

XX 23-MAR-2001; 2001US-277978P.

XX 25-MAY-2001; 2001US-293499P.

XX 12-MAR-1997; 97US-0815783.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Yu G, Ni J, Gentz RL, Dillon PJ;

XX WPI; 2002-556722/59.

XX N-PSDB; ABR88689.

XX WPI; 2002-066686/09.

DR Inhibiting activity of B cell maturation protein and/or transmembrane

XX activator and intracellular cyclophilin ligand interactor, by

PT administering a binding partner for APRIL, a tumor necrosis factor

PT family ligand

XX

PS Disclosure; Fig 2B; 94pp; English.

XX The invention relates to a method for inhibiting TACI (transmembrane

CC activator and intracellular CAML interactor) and/or B cell maturation

CC protein (BCMA) activity in a mammal. The method comprises administering

CC a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF

CC family ligand), having the consensus region of TACI, BCMA, or the TACI/

CC BCMA extracellular consensus sequence, but not the extracellular region

CC of TACI or BCMA. The method is useful for inhibiting activity of TACI

CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell

CC lymphoproliferative disorders, one or more solid tumours such as lung,

CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI

CC antagonists are useful for treating inflammation and immune function

CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic

CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung,

CC disease), drug and insect sting allergy, inflammatory bowel disease

CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple

CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,

CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer

CC with leucocyte infiltration of the skin or organs. The present sequence

CC is mouse FLAG-tagged soluble G70 protein.

XX

SO Sequence 149 AA;

Query Match 8.4%; Score 21; DB 23; Length 149;

Best Local Similarity 100.0%; Pred. No. 3.3e-12;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 204 PDRAYNSCYSGVFLHOGDI 224

Db 103 PDRAYNSCYSGVFLHOGDI 123

RESULT 46

AAO14137

ID AAO14137 standard; Protein; 176 AA.

XX

AC AAO14137;

XX

02-MAY-2002 (first entry)

DE Protein of a FLAG-tagged soluble extracellular domain of murine APRIL.

XX

Human transmembrane activator CAML interactor protein; TACI; cytosolic;

KW cell proliferation; tumour; vulvar; renal cell cancer; mastocytoma;

KW Kaposi's sarcoma; breast; ovarian carcinoma; rectal; throat; melanoma;

KW colon; bladder; mammary adenocarcinoma; gastrointestinal; hyperplasia;

KW pharyngeal squamous cell; stomach; cellular hyperproliferation; pannus;

KW scleroderma; rheumatoid arthritis; scarring; mean survival time; liver;

KW lung fibrosis; uric acid; murine; a proliferation inducing ligand; mouse;

KW APRIL; PS784; LT032.

XX

OS Mus sp.

XX

PH Key

FT 1..15 Location/Qualifiers

FT Peptide

FT 16..23 /note= "HA signal sequence"

FT 24..31 /note= "FLAG epitope"

FT 32..176 /note= "Short linker sequence, linking the FLAG epitope to the soluble murine APRIL sequence"

FT Region

FT /note= "Murine APRIL sequence"

PN WO200181417-A2.

XX

PD 01-NOV-2001.

XX

XX 27-APR-2001; 2001WO-US40626.

PF

XX 27-APR-2000; 2000US-199946P.

PR

XX

PA (BIOL) BIOGEN INC.

PA (APOT-) APOTEC R & D SA.

XX

PI Ambrose C, Thompson J, Schneider P, Rennert P;

XX

DR WPI; 2002-062027/08.

DR N-PSDB; AAK98733.

XX

PT Treating mammal for condition associated with undesired cell

PT proliferation e.g., solid tumour or reducing solid tumour size located in

PT protein reagent

XX

PS Examples; Fig 7; 42pp; English.

XX This sequence represents the protein encoded by the DNA of a FLAG-tagged

CC soluble extracellular domain of murine APRIL (A Proliferation Inducing

CC Ligand) as mapped in the mammalian expression plasmid PS784, also known

CC as LT032. The invention relates to treating a mammal for a condition

CC associated with undesired cell proliferation (e.g. a solid tumour, or

CC reducing the size of a solid tumour located on or in a mammal) comprising

CC administering a transmembrane activator CAML interactor protein (TACI)

CC reagent. The TACI reagent has cytosolic and vulvar activity. Treating

CC a mammal (e.g. human, cow, horse, dog, mouse, rat or cat) for a condition

CC associated with undesired cell proliferation (e.g. cancer such as renal

CC cell cancer, Kaposi's sarcoma, breast cancer, sarcoma, ovarian carcinoma,

CC rectal cancer, throat cancer, melanoma, colon cancer, bladder cancer,

CC mastocytoma, lung cancer, mammary adenocarcinoma, pharyngeal squamous

CC cell carcinoma, gastrointestinal cancer or stomach cancer). The method is

CC also useful for treating cellular hyperproliferation (hyperplasia) such

CC as scleroderma, pannus formation in rheumatoid arthritis, post-surgical

CC scarring and lung, liver and uterine fibrosis. The TACI reagent of the

CC invention can extend mean survival time of a mammal by 25% as compared to

CC the mean survival time of a mammal in the absence of administering the

CC TACI reagent. The TACI reagent also reduces the size of the tumour by 25%

CC or more.

XX

SO Sequence 176 AA;

Query Match 8.4%; Score 21; DB 23; Length 176;

Best Local Similarity 100.0%; Pred. No. 3.8e-12;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 204 PDRAYNSCYSGVFLHOGDI 224

Db 130 PDRAYNSCYSGVFLHOGDI 150

RESULT 47

AAE15503

ID AAE15503 standard; Protein; 199 AA.

XX

AC AAE15503;

XX

12-MAR-2002 (first entry)

DE Human-mouse APRIL G70 protein consensus sequence.

XX

XX Human; transmembrane activator and intracellular CAML interactor; TACI;

KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;

KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;

KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;

KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;

KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;

KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;

KW rheumatoid arthritis; atherosclerosis; APRIL G70.
 XX Homo sapiens.
 OS Mus sp.
 OS Mus sp.
 XX WO200187979-A2.
 PN 22-NOV-2001.
 PD 14-MAY-2001; 2001WO-US15567.
 PF 12-MAY-2000; 2000US-204039P.
 PR 27-JUN-2000; 2000US-214591P.
 PR 14-MAY-2001; 2001US-0214591.
 XX (AMGEN-) AMGEN INC.
 PA The11 LE, Yu G;
 PI WPI; 2002-066686/09.
 XX
 PT Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interact, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand -
 XX
 PS Disclosure; Fig 3; 94p; English.
 XX
 CC The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CML interact) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumors such as lung,
 CC gastrointestinal, pancreatic or prostate tumor. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma), hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human-mouse APRIL G70 protein consensus sequence.
 CC
 CC Sequence 199 AA;
 CC
 CC Query Match 8.4%; Score 21; DB 23; Length 199;
 CC Best Local Similarity 100.0%; Pred. No. 4.2e-12;
 CC Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 204 PDRVNSCYSGVPHLHOGDI 224
 CC |||||
 CC DB 158 PDRVNSCYSGVPHLHOGDI 178
 CC
 CC RESULT 48
 CC AAY04284
 CC ID AAY04284 standard; Protein; 232 AA.
 CC XX
 CC AC AAY04284;
 CC XX
 CC DT 17-JUN-1999 (first entry)
 CC XX
 CC DE Mouse APRIL protein sequence.
 CC XX
 CC KW APRIL; tumour necrosis factor; TNF; proliferating inducing agent;
 CC KW immune disorder; cancer.
 CC OS Mus sp.

XX WO9912965-A2.
 PN 18-MAR-1999.
 PD 11-SEP-1998; 98WO-US19191.
 PF 26-MAR-1998; 98US-0079384.
 PR 12-SEP-1997; 97US-0058786.
 XX (BIOD) BIOGEN INC.
 PA Techopp J;
 PI WPI; 1999-215028/18.
 DR N-PsDB; AAX30125.
 XX
 XX A Proliferating Inducing Agent (APRIL), a member of the Tumour
 PT Necrosis Factor family - useful as diagnostic agents and for
 PT prevention or treatment of immune disorders and cancer
 XX
 PS Disclosure; Page 47; 47p; English.
 XX
 CC The present sequence represents a proliferating inducing agent (APRIL)
 CC isolated from mouse. APRIL is a member of the tumour necrosis factor
 CC family, and essentially free of normally associated proteins. APRIL and
 CC APRIL antibodies are useful in pharmaceutical compositions for
 CC preventing or reducing severity of an autoimmune disease or an immune
 CC response to tissue graft. The composition is also useful for stimulating
 CC or suppressing the immune system, and treating cancer. APRIL is also
 CC useful for treating APRIL-related disorders by delivering via a vector
 CC (preferably viral vector) (gene therapy) into a mammalian (preferably
 CC human) cell. Labeled APRIL and fragments are useful for identifying
 CC APRIL receptors by screening compositions. Antisense DNA and antibodies
 CC and modified APRIL (preferably an anti-APRIL receptor antibody) are
 CC useful as blocking agents for inducing cell death by interfering with
 CC APRIL receptors. The blocking agent is preferably administered with
 CC interferon- γ , and treats, suppresses or alters an immune response
 CC involving a signalling pathway between APRIL and its receptor
 CC (preferably involving human carcinoma cells); and also treats,
 CC suppresses or alters the progression of cancer (preferably at least one
 CC chemotherapeutic agent is also administered, and radiation therapy is
 CC also given to the patient.
 CC
 CC Sequence 232 AA;
 CC
 CC Query Match 8.4%; Score 21; DB 20; Length 232;
 CC Best Local Similarity 100.0%; Pred. No. 4.8e-12;
 CC Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 204 PDRVNSCYSGVPHLHOGDI 224
 CC |||||
 CC DB 186 PDRVNSCYSGVPHLHOGDI 206
 CC
 CC RESULT 49
 CC AAY79672
 CC ID AAY79672 standard; Protein; 232 AA.
 CC XX
 CC AC AAY79672;
 CC XX
 CC DT 29-AUG-2000 (first entry)
 CC XX
 CC DE Mouse death receptor ligand-1 (DRL-1).
 CC XX
 CC KW DRL-1; mouse; death receptor ligand-1; tumour necrosis factor;
 CC KW TNF- γ ; TNF-like ligand; TLR; immunostimulant; immunosuppressive;
 CC KW T-cell response; transplant rejection; graft versus host disease;
 CC KW apoptosis.
 CC OS Mus sp.
 XX WO200026244-A2.

XX 11-MAY-2000.
PD 04-NOV-1999; 99WO-US25954.
XX 04-NOV-1998; 98US-0106976.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Leonardo M.J, Wang J, Jiang D;
PI WPI: 2000-365575/31.
DR N-PSDB; AAA27734.
XX Novel nucleic acids encoding tumor necrosis factor family polypeptides
PT termed as Death Receptor ligands useful for stimulating immune response
PT and inducing apoptosis comprising a specific nucleotide sequence -
XX Claim 20; Page 77; 80pp; English.
XX The present sequence is that of mouse death receptor ligand 1
CC (DRL-1), a novel member of the tumour necrosis factor (TNF) family,
CC also termed TNF-gamma or TNF-like ligand (TLL). The invention
CC provides human and murine DRL polypeptides, nucleic acids and
CC antibodies. DRL-1 polypeptides are used in claimed methods of
CC stimulating an immune response and of inducing apoptosis in a
CC population of T-cells. Antibodies to DRL-1 are used in claimed
CC methods of suppressing an immune response, inhibiting a T-cell
CC response associated with transplant rejection or graft versus host
CC disease, inhibiting apoptosis in a population of T cells, and of
CC stimulating the membrane-bound form of DRL-1.
SQ Sequence 232 AA;
Query Match 8.4%; Score 21; DB 21; Length 232;
Best Local Similarity 100.0%; Pred. No. 4.8e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 204 PDRAYNSCYSAGVFHLHGDI 224
Db 186 PDRAYNSCYSAGVFHLHGDI 206
RESULT 50
AAE07878
ID AAE07878 standard; Protein; 232 AA.
XX AAE07878;
AC
DE 01-NOV-2001 (first entry)
XX Mouse APRIL protein.
XX Mouse; tumour necrosis factor; TNF; ABBF; APRIL; BAF; therapy; melanoma;
XX immune system-related disorder; cancer; renal cell; breast; stomach;
XX rectal; colon; throat; bladder; ovarian carcinoma; cellular disorder;
XX gastrointestinal; scleroderma; Kaposi's sarcoma; chronic leukaemia;
XX squamous cell carcinoma; hyperproliferative condition; pannus formation;
XX rheumatoid arthritis; postsurgical scarring; fibrosis; liver; uterine;
XX lung; immunodeficiency; inflammatory disease; lymphadenopathy; vulnary;
XX autoimmune disease; graft versus host disease; dermatological;
XX antiinflammatory; immunosuppressive; cytostatic.
OS Mus sp.
XX
XX Key Location/Qualifiers
FT Misc-difference 133 /note= "Encoded by CCA"
FT Misc-difference 134..135 /note= "Encoded by GGGAGAC"
XX
XX WO200158949-A2.

PD 16-AUG-2001.
XX 08-FEB-2001; 2001WO-US04121.
XX 11-FEB-2000; 2000US-0181670.
XX (BIOJ) BIOGEN INC.
XX Renner PD, Thompson JS, Ambrose C, Cachero TG;
PI WPI: 2001-514644/56.
DR N-PSDB; AAD14416.
XX New heteromeric ligand of tumor necrosis factor (TNF) family, useful
PT for diagnosis, treatment of immune system-related disorders in humans,
PT comprises TNF-family member APRIL subunit linked non-covalently to
PT TNF-family member BAF subunit -
XX Claim 2; Fig 1e; 42pp; English.
XX The present invention relates to an isolated heteromeric ligand of
CC tumour necrosis factor (TNF)-family, referred to as ABBF comprising a
CC TNF-family member APRIL subunit linked non-covalently to TNF-family
CC member BAF subunit. ABBF is useful for diagnosis or treatment of
CC various immune system-related disorders in mammals, preferably humans.
CC Such disorders include cancer, including cellular disorders, for e.g.
CC renal cell cancer, Kaposi's sarcoma, chronic leukaemia, breast cancer,
CC colon cancer, ovarian carcinoma, rectal cancer, throat cancer, melanoma,
CC colorectal cancer, bladder cancer, squamous cell carcinoma and
CC gastrointestinal or stomach cancer, cellular hyperproliferative
CC conditions, such as scleroderma, pannus formation in rheumatoid
CC arthritis, postsurgical scarring and lung, liver and uterine fibrosis
CC and immunodeficiencies, inflammatory diseases, lymphadenopathy,
CC autoimmune diseases and graft versus host disease. ABBF is also useful
CC for producing monoclonal or polyclonal antibodies and for identifying
CC novel modulators affecting biological function and receptors interacting
CC with ABBF. The present sequence is mouse APRIL protein.
XX
SQ Sequence 232 AA;
Query Match 8.4%; Score 21; DB 22; Length 232;
Best Local Similarity 100.0%; Pred. No. 4.8e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 204 PDRAYNSCYSAGVFHLHGDI 224
Db 186 PDRAYNSCYSAGVFHLHGDI 206
RESULT 51
AAE0504
ID AAE0504 standard; Protein; 234 AA.
XX AAE0504;
AC
XX 31-JUL-2001 (first entry)
XX Murine myc tagged A Proliferation Inducing Ligand (APRIL).
XX Murine; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
XX gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
XX carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
XX systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
XX B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
XX organ transplantation; KIL motif; HIV; human immunodeficiency virus;
XX tumour necrosis factor; TNF; BCMA; B cell maturation protein; myc tag.
XX
XX Mus sp.
XX Synthetic.
XX Key Location/Qualifiers
FT Region 86..96 /label= Myc_tag
FT

FT Domain 97..99
 FT /label= KEl_motif
 FT /note= "This motif is from FAS ligand"
 XX
 PN MO200124811-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US27579.
 XX
 PR 06-OCT-1999; 99US-0157933.
 PR 11-FEB-2000; 2000US-0181807.
 PR 30-JUN-2000; 2000US-0215688.
 XX
 PA (BIOJ) BIOGEN INC.
 PA (APOT-) APOTEC R & D SA.
 XX
 PI Schneider P, Thompson J, Cachero T, Ambrose C, Rennett P;
 XX
 WP1; 2001-266242/27.
 N-PSDB; AAD03840.
 XX
 PT Treating a mammal for a condition associated with undesired cell
 PT proliferation such as cancer or carcinoma, comprises administering a
 PT composition comprising A Proliferation Inducing Ligand Receptor
 PT (APRIL-R) antagonist
 XX
 PS Example 1; Fig 1; 85pp; English.
 XX
 CC The invention relates to a method of treating a mammal for a condition
 CC associated with undesired cell proliferation such as cancer or
 CC carcinoma. The method involves administering a composition comprising
 CC A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as
 CC B cell maturation protein (BCM or BCMA) antagonist that antagonises the
 CC interaction between APRIL and its cognate receptor(s). This method is
 CC useful for treating undesired cell proliferation such as cancer or
 CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,
 CC prostate carcinoma, and other carcinomas whose proliferation is modulated
 CC by APRIL. It is also useful for treating autoimmune diseases (grave's
 CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular
 CC diseases, renal disorders, B-cell lympho-proliferative disorders,
 CC immunosuppressive diseases, organ transplantation, inflammation and
 CC human immunodeficiency virus (HIV), and for treating, suppressing or
 CC altering an immune response involving a signalling pathway between
 CC APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy.
 CC The present sequence is murine A Proliferation Inducing Ligand (APRIL)
 CC protein. This sequence comprises myc epitope and KEl motif from FAS
 CC ligand followed by APRIL extracellular domain. APRIL is a member of
 CC Tumour Necrosis Factor (TNF) family of proteins.
 CC
 CC Sequence 234 AA;
 SQ
 XX
 Query Match 8.4%; Score 21; DB 22; Length 234;
 Best Local Similarity 100.0%; Pred. No. 4.9e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 204 PDRAYNSCYSAGVPHLHOGDI 224
 ||||||||||||||||
 DB 188 PDRAYNSCYSAGVPHLHOGDI 208
 ||||||||||||||||
 RESULT 52
 ID AAE15483 standard; Protein; 240 AA.
 XX
 AC AAE15483;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Mouse APRIL/G70 protein.
 XX
 KW Mouse; transmembrane activator and intracellular CAML interactor; TACI;
 KW cyotabatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;

KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis; APRIL G70.
 XX
 OS Mus sp.
 XX
 PN MO200187979-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 14-MAY-2001; 2001WO-US15567.
 XX
 PR 12-MAY-2000; 2000US-204039P.
 PR 27-JUN-2000; 2000US-214591P.
 PR 14-MAY-2001; 2001US-0214591.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Theill LE, Yu G;
 XX
 DR WP1; 2002-066686/09.
 N-PSDB; AAD24709.
 XX
 PT Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor
 PT family ligand
 XX
 PS Disclosure; Fig 2B; 94pp; English.
 XX
 CC The invention relates to a method for inhibiting TACI (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering
 CC a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
 CC and/or BCMA in a mammal which is useful for creating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis), systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is mouse APRIL G70 protein.
 CC
 CC Sequence 240 AA;
 SQ
 XX
 Query Match 8.4%; Score 21; DB 23; Length 240;
 Best Local Similarity 100.0%; Pred. No. 5e-11;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 204 PDRAYNSCYSAGVPHLHOGDI 224
 ||||||||||||||||
 DB 194 PDRAYNSCYSAGVPHLHOGDI 214
 ||||||||||||||||
 RESULT 53
 ID AAW93589 standard; Protein; 241 AA.
 XX
 AC AAW93589;
 XX
 DT 18-JUN-1999 (first entry)
 XX
 DE Mouse TNFR1-beta protein.

```

XX      Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW      developmental abnormality; gestational abnormality; prostate cancer;
KW      APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW      cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW      apoptosis; mouse; TNRL1-beta.
XX
OS      Mus sp.
XX
PN      WO9911791-A2.
XX
PD      11-MAR-1999.
XX
PF      04-SEP-1998; 98WO-US18393.
XX
PR      05-SEP-1997; 97US-0924634.
XX
PA      (UNIW ) UNIV WASHINGTON.
XX
Chaudhary PM;
XX
WPI; 1999-205191/17.
DR      N-PSDB; AAX23423.
XX
PT      New Tumor Necrosis Factor family receptor polypeptides and ligands -
PT      useful for diagnosis and treatment of prostate cancer and
PT      developmental or gestational abnormalities
XX
PS      Claim 35; Fig 12B; 156pp; English.
XX
CC      This invention describes isolated Tumor Necrosis Factor (TNF) family
CC      receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
CC      fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
CC      their active fragments. APO4 is useful for diagnosing prostate cancer
CC      by determining levels of APO4 in an individual. Prostate cancer can also
CC      be treated using APO4 selective binding agents linked to a therapeutic
CC      moiety. APO4 polypeptides are also useful for identifying selective
CC      binding agents, useful in diagnosis/treatment of disease by binding of
CC      agents to the polypeptide/active fragment which is extracellular, or
CC      expressed on the cell surface. The binding is preferably performed in
CC      vivo. APO4 polypeptides/active fragments are also useful for screening in
CC      for agonists and antagonists by binding and observing the change in APO4
CC      activity. Effective pharmacological agents useful in diagnosis or
CC      treatment of disease are also identified using APO4 polypeptides/active
CC      fragments and APO4 signal transducer molecules that specifically interact
CC      with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC      activity. The method is performed in vivo or in vitro. APO polypeptides
CC      are all useful as immunogens for preparing antibodies. APO4 is also
CC      useful for diagnosis/treatment of developmental or gestational
CC      abnormalities. APO8 was transfected to human breast carcinoma cell line
CC      MCF-7, and induced apoptosis.
XX
SQ      Sequence 241 AA;
XX
Query Match 8.4%; Score 21; DB 20; Length 241;
Best Local Similarity 100.0%; Pred. No. 5e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

KW      Human transmembrane activator CAML interactor protein; TACI; cytostatic;
KW      cell proliferation; tumour; vulnery; renal cell cancer; mastocytoma;
KW      Kaposi's sarcoma; breast; ovarian carcinoma; rectal; throat; melanoma;
KW      colon; bladder; mammary adenocarcinoma; gastrointestinal; hyperplasia;
KW      pharyngeal squamous cell; stomach; cellular hyperproliferation; pannus;
KW      scleroderma; rheumatoid arthritis; scarring; mean survival time; liver;
KW      lung fibrosis; uterine; murine; a proliferation inducing ligand; mouse;
KW      APRIL; chimeric.
XX
OS      Chimeric - Mus sp.
XX
OS      Chimeric - unidentified.
XX
FH      Key
XX      Location/Qualifiers
FT      Region
XX      86..96
FT      /label= Myc_epitope
XX      97..104
FT      /label= Short_linker_region
XX      105..249
FT      Domain
XX      /label= Extracellular_domain
XX      /note= "Extracellular domain of the murine APRIL coding
XX      sequence"
XX
PN      WO200181417-A2.
XX
PD      01-NOV-2001.
XX
PF      27-APR-2001; 2001WO-US40626.
XX
PR      27-APR-2000; 2000US-199946P.
XX
PA      (BIOJ ) BIOGEN INC.
XX      (ABOT-) APOTEC R & D SA.
XX
PI      Ambrose C, Thompson J, Schneider P, Rennett P;
XX
WPI; 2002-062027/08.
DR      N-PSDB; AAK98727.
XX
PT      Treating mammal for condition associated with undesired cell
PT      proliferation e.g., solid tumour or reducing solid tumour size located in
PT      mammal comprises administering transmembrane activator CAML interactor
PT      protein reagent -
XX
PS      Examples; Fig 6; 42pp; English.
XX
CC      This sequence represents the protein of a myc-tagged murine APRIL (A
CC      proliferation inducing ligand) construct. The invention relates to
CC      treating a mammal for a condition associated with undesired cell
CC      proliferation (e.g. a solid tumour, or reducing the size of a solid
CC      tumour located on or in a mammal) comprising administering a
CC      transmembrane activator CAML interactor protein (TACI) reagent. The TACI
CC      reagent has cytostatic and vulnery activity. Treating a mammal (e.g.
CC      human, cow, horse, dog, mouse, rat or cat) for a condition associated
CC      with undesired cell proliferation (e.g. cancer such as renal cell cancer,
CC      Kaposi's sarcoma, breast cancer, sarcoma, ovarian carcinoma, rectal
CC      cancer, throat cancer, melanoma, colon cancer, bladder cancer,
CC      mastocytoma, lung cancer, mammary adenocarcinoma, pharyngeal squamous
CC      cell carcinoma, gastrointestinal cancer or stomach cancer). The method is
CC      also useful for treating cellular hyperproliferation (hyperplasia) such
CC      as scleroderma, pannus formation in rheumatoid arthritis, post-surgical
CC      scarring and lung, liver and uterine fibroids. The TACI reagent of the
CC      invention can extend mean survival time of a mammal by 25% as compared to
CC      the mean survival time of a mammal in the absence of administering the
CC      TACI reagent. The TACI reagent also reduces the size of the tumour by 25%
CC      or more.
XX
SQ      Sequence 249 AA;
XX
Query Match 8.4%; Score 21; DB 23; Length 249;
Best Local Similarity 100.0%; Pred. No. 5.1e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```


Db 203 PDRAYNSCYSAQVFLHGGDI 223

RESULT 55

AA662328 standard; peptide; 15 AA.

29-JUN-2001 (first entry)

Human TRDL-1gamma peptide epitope (residues 121-135).

Tumour necrosis factor related death ligand-1gamma; TRDL-1gamma; TRDL; cell death; apoptosis; human; epitope.

Synthetic.
Homo sapiens.

MO200125256-A2.

12-APR-2001.

06-OCT-2000; 2000WO-US27866.

06-OCT-1999; 99US-0157913.

(UTAH) UNIV UTAH RES FOUND.

Jones D, Manos E;

WPI; 2001-281728/29.

Isolated and purified polynucleotide encoding human tumor necrosis factor related death ligand (TRDL)-1 gamma useful for identifying agents that inhibit or enhance TRDL-1 gamma mediated induction of apoptosis -

Example 6; Page 15; 39pp; English.

The invention provides a human tumor necrosis factor related death ligand-1gamma (TRDL-1gamma). The TRDL-1gamma polypeptide can be expressed by standard recombinant methodology. TRDL-1gamma stimulates Jurkat cell death. It is useful for identifying agents capable of inhibiting or enhancing TRDL-1gamma mediated induction of apoptosis. The present sequence represents a TRDL-1gamma peptide epitope, used for generating rabbit polyclonal antibodies.

Sequence 15 AA;

Query Match 5.6%; Score 14; DB 22; Length 15;

Best Local Similarity 100.0%; Pred. NO. 2.8e-06; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 PINATSKDSDVTE 135

Db 2 PINATSKDSDVTE 15

RESULT 56

AA607407 standard; Protein; 184 AA.

AA607407;

17-OCT-2000 (first entry)

Arabidopsis thaliana protein fragment SEQ ID NO: 4549.

Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

XX Arabidopsis thaliana.

OS EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 25-MAR-1999; 99US-0126264.

XX 29-MAR-1999; 99US-0126785.

XX 01-APR-1999; 99US-0127462.

XX 06-APR-1999; 99US-0128234.

XX 08-APR-1999; 99US-0128714.

XX 16-APR-1999; 99US-0129845.

XX 19-APR-1999; 99US-0130077.

XX 21-APR-1999; 99US-0130449.

XX 23-APR-1999; 99US-0130510.

XX 23-APR-1999; 99US-0130991.

XX 28-APR-1999; 99US-0131449.

XX 30-APR-1999; 99US-0132048.

XX 04-MAY-1999; 99US-0132407.

XX 05-MAY-1999; 99US-0132485.

XX 06-MAY-1999; 99US-0132486.

XX 06-MAY-1999; 99US-0132487.

XX 07-MAY-1999; 99US-0132863.

XX 11-MAY-1999; 99US-0134256.

XX 14-MAY-1999; 99US-0134218.

XX 14-MAY-1999; 99US-0134221.

XX 14-MAY-1999; 99US-0134370.

XX 18-MAY-1999; 99US-0134768.

XX 19-MAY-1999; 99US-0134941.

XX 20-MAY-1999; 99US-0135124.

XX 21-MAY-1999; 99US-0135353.

XX 24-MAY-1999; 99US-0135629.

XX 25-MAY-1999; 99US-0136021.

XX 27-MAY-1999; 99US-0136392.

XX 28-MAY-1999; 99US-0136782.

XX 01-JUN-1999; 99US-0137222.

XX 03-JUN-1999; 99US-0137528.

XX 04-JUN-1999; 99US-0137502.

XX 07-JUN-1999; 99US-0137724.

XX 08-JUN-1999; 99US-0138094.

XX 10-JUN-1999; 99US-0138540.

XX 10-JUN-1999; 99US-0138647.

XX 14-JUN-1999; 99US-0139119.

XX 16-JUN-1999; 99US-0139452.

XX 16-JUN-1999; 99US-0139453.

XX 17-JUN-1999; 99US-0139454.

XX 18-JUN-1999; 99US-0139454.

XX 18-JUN-1999; 99US-0139455.

XX 18-JUN-1999; 99US-0139456.

XX 18-JUN-1999; 99US-0139457.

XX 18-JUN-1999; 99US-0139458.

XX 18-JUN-1999; 99US-0139459.

XX 18-JUN-1999; 99US-0139460.

XX 18-JUN-1999; 99US-0139461.

XX 18-JUN-1999; 99US-0139462.

XX 18-JUN-1999; 99US-0139463.

XX 18-JUN-1999; 99US-0139750.

XX 18-JUN-1999; 99US-0139763.

XX 21-JUN-1999; 99US-0139817.

XX 22-JUN-1999; 99US-0139899.

XX 23-JUN-1999; 99US-0140353.

XX 23-JUN-1999; 99US-0140354.

XX 24-JUN-1999; 99US-0140695.

XX 28-JUN-1999; 99US-0140823.

PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141849.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145275.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147202.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149902.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.

PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0156599.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158212.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159894.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 3.2%; Score 8; DB 21; Length 184;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 36 GALLGAVA 43
DB 25 GALLGAVA 32

RESULT 57
AAG07406
ID AAG07406 standard; Protein: 223 AA.
XX AAG07406;
AC
XX 17-OCT-2000 (first entry)
DT
XX Arabidopsis thaliana protein fragment SEQ ID NO: 4548.
DE
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
OS Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX

PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-011825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126266.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132485.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134766.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138099.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139452.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139889.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140822.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141847.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.

PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.

PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
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 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161922.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 3.2%; Score 8; DB 21; Length 223;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 GAALGAVA 43
 ID |||||
 DB 64 GAALGAVA 71

RESULT 58

AAU90178 standard; Peptide; 20 AA.

AC AAU90178;
 XX 18-JUN-2002 (first entry)
 XX Insulin/insulin-like growth factor receptor-binding peptide #2134.
 DE Insulin/insulin-like growth factor receptor-binding peptide #2134.
 XX
 KW Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
 KW ophthalmological; insulin; receptor; gene therapy; diabetes;
 KW insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
 KW diabetic retinopathy; neurological diseases; stroke;
 KW diabetic neuropathy.
 XX
 OS Synthetic.
 XX
 PN WO200172771-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 29-MAR-2000; 2000WO-US08528.
 XX
 PR 29-MAR-2000; 2000WO-US08528.
 XX
 PA (DGIB-) DGI BIOTECHNOLOGIES LLC.

PA (NOVO) NOVO NORDISK AS.
 XX Beasley J, Blume AJ, Schaeffer L, Pillutia R, Brandt J;
 PI Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandeckl WS;
 PI Hansen PH, Ravera M, Hsiao K;
 DR WPI; 2002-025774/03.
 XX
 PT Modulating insulin activity in mammalian cells, for treating e.g.
 PT diabetes and tumours, comprises using peptides that bind to insulin or
 PT insulin-like growth factor receptors
 PS Disclosure; Figure 4C; 390pp; English.
 XX
 CC The invention relates to a method of modulating insulin activity in
 CC mammalian cells by administering a peptide that binds the insulin
 CC receptor (IR). A composition containing a peptide, optionally expressed
 CC from gene therapy vectors, that binds to Site 1 of IR and an insulin
 CC agonist are useful for treating diabetes. Also, peptides that are
 CC antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
 CC useful for treating insulin-like growth factor (IGF)-sensitive tumours
 CC (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
 CC receptor agonists are useful for treating neurological diseases,
 CC including stroke and diabetic neuropathy. The peptides are also useful in
 CC screening for compounds that bind to IR or IGF-1 receptor, potential
 CC therapeutics and research reagents. AAU88034-AAU90957 represent IR
 CC and/or IGF-1 receptor-binding peptides and related amino acid sequences
 CC of the invention.
 XX
 SQ Sequence 20 AA;

Query Match 2.8%; Score 7; DB 23; Length 20;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 LSWGAL 39
 ID |||||
 DB 8 LSWGAL 14

RESULT 59

AAU90722 standard; Peptide; 20 AA.

ID AAU90722
 XX
 AC AAU90722;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Insulin/insulin-like growth factor receptor-binding peptide #2678.
 XX
 KW Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
 KW ophthalmological; insulin; receptor; gene therapy; diabetes;
 KW insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
 KW diabetic retinopathy; neurological diseases; stroke;
 KW diabetic neuropathy.
 XX
 OS Synthetic.
 XX
 PN WO200172771-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 29-MAR-2000; 2000WO-US08528.
 XX
 PR 29-MAR-2000; 2000WO-US08528.
 XX
 PA (DGIB-) DGI BIOTECHNOLOGIES LLC.
 PA (NOVO) NOVO NORDISK AS.
 XX
 PI Beasley J, Blume AJ, Schaeffer L, Pillutia R, Brandt J;
 PI Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandeckl WS;
 PI Hansen PH, Ravera M, Hsiao K;

DR WPI: 2003-025774/03.
XX Modulating insulin activity in mammalian cells, for treating e.g.
PT diabetes and tumors, comprises using peptides that bind to insulin or
XX insulin-like growth factor receptors -
PS Disclosure; Figure 11B; 390pp; English.
XX
CC The invention relates to a method of modulating insulin activity in
CC mammalian cells by administering a peptide that binds the insulin
CC receptor (IR). A composition containing a peptide, optionally expressed
CC from gene therapy vectors, that binds to Site 1 of IR and an insulin
CC agonist are useful for treating diabetes. Also, peptides that are
CC antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
CC useful for treating insulin-like growth factor (IGF)-sensitive tumors
CC (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
CC receptor agonists are useful for treating neurological diseases,
CC including stroke and diabetic neuropathy. The peptides are also useful in
CC screening for compounds that bind to IR or IGF-1 receptor, potential
CC therapeutics and research reagents. AAU88034-AAU90957 represent IR
CC and/or IGF-1 receptor-binding peptides and related amino acid sequences
XX of the invention.
SQ Sequence 20 AA;
XX
Query Match 2.8%; Score 7; DB 23; Length 20;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 33 LSMGAL 39
DB 8 LSMGAL 14
XX
RESULT 60
AAB18725
ID AAB18725 standard; Protein; 27 AA.
XX
AC AAB18725;
XX
DT 22-JAN-2001 (first entry)
XX
DE Amino acid sequence of mature protein dermaseptin b.
XX
KW Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant;
XX cationic peptide; pathogen resistance.
XX
OS Phyllomedusa bicolor.
XX
WO200055337-A1.
XX
PD 21-SEP-2000.
XX
PF 16-MAR-2000; 2000WO-CA00288.
XX
PR 17-MAR-1999; 99US-0125072.
XX
PA (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
XX
PI Misra S, Kay WD.
XX
DR WPI: 2000-647077/62.
XX
PT Transgenic plants resistant to broad spectrum of pathogens useful for
PT producing biologically active cationic peptides, comprises nucleic acid
PT molecule encoding temporin and/or dermaseptin peptides -
XX
XX
XX Claim 3; Page 47; 58pp; English.
XX
PS AAB18725-36 represent mature processed forms of dermaseptin. Dermaseptin
PS has antibacterial activity, and inhibits fungal growth. Cationic
PS peptides derived from temporins and dermaseptins are used to produce
PS transgenic plants. The transgenic plants are useful for producing
PS biologically active cationic peptides such as temporins and dermaseptins
PS in large quantities. The peptide confers broad spectrum pathogen
PS resistance including enhanced resistance to both fungal and bacterial
PS pathogens in the transgenic plants. The transgenic plants may be used
PS in conventional agricultural applications such as food crops, medical
PS and other applications.
XX
SQ Sequence 31 AA;
XX
Query Match 2.8%; Score 7; DB 21; Length 31;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 37 AALGAVA 43
DB 20 AALGAVA 26

CC biologically active cationic peptides such as temporins and dermaseptins
CC in large quantities. The peptide confers broad spectrum pathogen
CC resistance including enhanced resistance to both fungal and bacterial
CC pathogens in the transgenic plants. The transgenic plants may be used
CC in conventional agricultural applications such as food crops, medical
CC and other applications.
XX
SQ Sequence 27 AA;
XX
Query Match 2.8%; Score 7; DB 21; Length 27;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 37 AALGAVA 43
DB 16 AALGAVA 22
XX
RESULT 61
AAB18726
ID AAB18726 standard; Protein; 31 AA.
XX
AC AAB18726;
XX
DT 22-JAN-2001 (first entry)
XX
DE Amino acid sequence of mature protein dermaseptin B.
XX
KW Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant;
XX cationic peptide; pathogen resistance.
XX
OS Phyllomedusa bicolor.
XX
PN WO200055337-A1.
XX
PD 21-SEP-2000.
XX
PF 16-MAR-2000; 2000WO-CA00288.
XX
PR 17-MAR-1999; 99US-0125072.
XX
PA (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
XX
PI Misra S, Kay WD.
XX
DR WPI: 2000-647077/62.
XX
PT Transgenic plants resistant to broad spectrum of pathogens useful for
PT producing biologically active cationic peptides, comprises nucleic acid
PT molecule encoding temporin and/or dermaseptin peptides -
XX
XX
XX Claim 3; Page 47; 58pp; English.
XX
PS AAB18725-36 represent mature processed forms of dermaseptin. Dermaseptin
PS has antibacterial activity, and inhibits fungal growth. Cationic
PS peptides derived from temporins and dermaseptins are used to produce
PS transgenic plants. The transgenic plants are useful for producing
PS biologically active cationic peptides such as temporins and dermaseptins
PS in large quantities. The peptide confers broad spectrum pathogen
PS resistance including enhanced resistance to both fungal and bacterial
PS pathogens in the transgenic plants. The transgenic plants may be used
PS in conventional agricultural applications such as food crops, medical
PS and other applications.
XX
SQ Sequence 31 AA;
XX
Query Match 2.8%; Score 7; DB 21; Length 31;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 37 AALGAVA 43
DB 20 AALGAVA 26

RESULT 62

AAB12436

ID AAB12436 standard; peptide; 31 AA.

XX AAB12436;

DT 20-OCT-2000 (first entry)

DE Dermaseptin B amino acid sequence.

XX CEMA; Pro-CEMA; dermaseptin B; temporin A; cecropin A; melittin;

XX CAMA 35S promoter; cationic polypeptide; antimicrobe; transgenic plant;

XX expression vector; agrobacillus; callus; phytopathogen; bacteria;

XX fungus; calli; antifungal; antibacterial.

XX Unidentified.

XX CN1249310-A.

XX 05-APR-2000.

XX 28-SEP-1998; 98CN-0112269.

XX 28-SEP-1998; 98CN-0112269.

XX (ZHOU) ZHOU G.

XX Zhou G;

XX WPI; 2000-400710/35.

XX Cationic polypeptide process for expressing antimicrobe in plant -

XX Claim 2; Page 1; 7pp; Chinese.

XX The present invention describes a transgenic plant expression vector

XX containing three antimicrobial cationic polypeptides. The plant tissue is

XX introduced to these genes via agrobacillus and in the callus culture,

XX the callus resisting phytopathogen (bacteria and fungus) can be

XX externally chosen. Choosing these calli can regenerate plants and

XX directly test its antifungal and antibacterial powder. After these

XX transgenic plants are ripened, whole or partial plant can be harvested.

XX The present sequence represents a specifically claimed peptide from

XX the present invention.

XX Sequence 31 AA;

XX Query Match 2.8%; Score 7; DB 21; Length 31;

XX Best Local Similarity 100.0%; Pred. No. 33;

XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 37 AALGAVA 43

XX DB 20 AALGAVA 26

XX A mature dermaseptin protein with a N-terminal extension.

XX Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant;

XX cationic peptide; pathogen resistance.

XX Synthetic.

XX Phylomedusa bicolor.

XX WO20005337-A1.

XX 21-SEP-2000.

XX 16-MAR-2000; 2000WO-CA00288.

XX 17-MAR-1999; 99US-0125072.

XX (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.

XX Miera S, Kay WD;

XX WPI; 2000-647077/62.

XX N-PSDB; AAA75751.

XX Transgenic plants resistant to broad spectrum of pathogens useful for

XX producing biologically active cationic peptides, comprises nucleic acid

XX molecule encoding temporin and/or dermaseptin peptides -

XX Example; Page 51; 58pp; English.

XX The present sequence represents a mature dermaseptin polypeptide

XX which has a N-terminal extension. Dermaseptin has antibacterial

XX activity, and inhibits fungal growth. Cationic peptides derived from

XX temporins and dermaseptins are used to produce transgenic plants. The

XX transgenic plants are useful for producing biologically active cationic

XX peptides such as temporins and dermaseptins in large quantities. The

XX peptide confers broad spectrum pathogen resistance including enhanced

XX resistance to both fungal and bacterial pathogens in the transgenic

XX plants. The transgenic plants may be used in conventional agricultural

XX applications such as food crops, medical and other applications.

XX Sequence 32 AA;

XX Query Match 2.8%; Score 7; DB 21; Length 32;

XX Best Local Similarity 100.0%; Pred. No. 34;

XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 37 AALGAVA 43

XX DB 21 AALGAVA 27

XX Promoter; lipase gene; Burkholderia genus microbe; lipase production.

XX Pseudomonas cepacia.

XX JP09322776-A.

XX 16-DEC-1997.

XX 31-MAY-1996; 96JP-0160637.

XX 31-MAY-1996; 96JP-0160637.

XX (CHCC) CHISSO CORP.

XX WPI; 1998-094675/09.

XX N-PSDB; AAT99136.

XX Recombinant plasmid used to prepare lipase - using host-vector

XX system for Burkholderia genus microbe

XX Claim 6; Page 8; 12pp; Japanese.
PS
CC This sequence represents the lipase signal peptide. The lipase gene
CC promoter region can be used in the plasmid of the invention. The plasmid
CC of the invention is a recombinant plasmid in which a DNA fragment
CC containing the promoter region of the lipase gene (comprising a sequence
CC encoding a signal peptide) and a gene controlling lipase activity
CC to transform a Burkholderia genus microbe, which is then cultured to
CC produce a recombinant lipase. The recombinant lipase can be prepared in
CC large amounts.
XX
SQ Sequence 45 AA;
Query Match 2.8%; Score 7; DB 19; Length 45;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
40 GAVACAM 46
12 GAVACAM 18
RESULT 65
AAM86507
ID AAM86507 standard; Protein; 61 AA.
XX
AC AAM86507;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen SEQ ID NO:14100.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytosol; gene therapy; vaccine; metastasis.
XX
OS Homo sapiens.
XX
PN WQ200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 02-MAR-2000; 2000US-0184664.
PR 16-MAR-2000; 2000US-0186350.
PR 17-MAR-2000; 2000US-0189874.
PR 18-APR-2000; 2000US-0190076.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 11-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0217496.
PR 26-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0230963.
PR 14-AUG-2000; 2000US-0234518.
PR 14-AUG-2000; 2000US-0234519.
PR 14-AUG-2000; 2000US-0235213.
PR 14-AUG-2000; 2000US-0235214.
PR 14-AUG-2000; 2000US-0235266.
PR 14-AUG-2000; 2000US-0235267.
PR 14-AUG-2000; 2000US-0235268.
PR 14-AUG-2000; 2000US-0235270.
PR 14-AUG-2000; 2000US-0235447.
PR 14-AUG-2000; 2000US-0235757.

PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229345.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.

PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 05-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251889.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0235678.
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 DR WPI: 2001-483426/52.
 DR N-PSDB; AAK59288.
 XX
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis -
 PT
 XX
 Claim 11; SEQ ID NO 14100; 3071bp + Sequence Listing; English.

CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAK62170 to AAK61921. (I) have cytostratic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK67694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK62169
 CC represent sequences used in the exemplification of the present invention.
 CC
 XX
 SQ Sequence 61 AA;

Query Match 2.8%; Score 7; DB 22; Length 61;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 97 GERSRKR 103
 DB 6 GERSRKR 12
 RESULT 66
 AAB16374
 ID AAB16374 standard; Protein; 62 AA.
 XX
 AC AAB16374;
 XX
 DT 24-OCT-2000 (first entry)
 XX
 DE Eucalyptus grandis diphenol oxidase protein sequence SEQ ID NO:300.
 XX
 KW Plant; lignin; lignin biosynthetic pathway; Eucalyptus grandis;
 KW Pinus radiata; Monterey pine.
 XX
 OS Eucalyptus grandis.
 XX
 PN WO20002209-A1.
 XX
 PD 20-APR-2000.
 XX
 PF 06-OCT-1999; 99WO-N200168.
 XX
 PR 09-OCT-1998; 98US-0169789.
 PR 14-JUL-1999; 99US-0143811.
 XX
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 XX (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 XX
 PI Bloksberg LN, Havukkala JU;
 XX
 DR WPI: 2000-317962/27.
 XX
 PT Novel polynucleotide encoding enzymes involved in lignin-biosynthetic
 PT pathway useful for producing transgenic plants especially eucalyptus
 PT and pine species having altered lignin content, composition and
 PT structure -
 PT
 XX
 XX
 PS Claim 18; Page 156; 213pp; English.

CC The present invention describes isolated polynucleotides and proteins
 CC encoding and representing the enzymes cinnamate 4-hydroxylase (C4H),
 CC coumarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase
 CC (OMT), cinnamyl alcohol dehydrogenase (CAD), cinnamoyl-CoA reductase
 CC (CCR), phenylalanine ammonia-lyase (PAL), 4-coumarate:CoA ligase (4CL),
 CC coniferol glucosyl transferase (CGT), coniferin beta-glucosidase (CBG),
 CC laccase, peroxidase, ferulate-5-hydroxylase (F5H), alpha-amylase,
 CC caffeic acid methyl transferase, caffeoyl CoA methyl transferase,
 CC coumarate CoA ligase, cytochrome P450 LXXIA, diphenol oxidase, flavanol
 CC glucosyl transferase, flavonoid hydroxylase, and isochlorogenic reductase,
 CC which are involved in the lignin biosynthetic pathway. The
 CC polynucleotides can be used for modulating lignin content, lignin
 CC composition and the structure of a plant, especially eucalyptus and pine
 CC species, and for modifying the activity of an enzyme involved in lignin
 CC biosynthetic pathway, and for producing a plant having altered lignin
 CC content, composition, and structure. They can be used for designing probes
 CC and primers useful for detecting similar DNA and RNA sequences in any
 CC organism and for PCR amplification. The lignin content can be efficiently
 CC modified using the polynucleotides. AAK67908 to AAK68201 and AAB16341 to
 CC AAB16449 represent polynucleotide and protein sequences used in the
 CC exemplification of the present invention.
 CC
 XX
 SQ Sequence 62 AA;

Query Match 2.8%; Score 7; DB 21; Length 62;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 242 GTTGGFV 248
 |||||

Db 5 GTFB3FV 11

RESULT 67

ABG12905
ID ABG12905 standard; Protein: 65 AA.

XX ABG12905;

DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #12896.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KM food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

11-OCT-2001.

30-MAR-2001; 2001WO-US08631.

31-MAR-2000; 2000US-0540217.

23-AUG-2000; 2000US-0649167.

(HYSE-) HYSEQ INC.

Drmanac RT, Liu C, Tang YT;

WPI; 2001-639362/73.

N-PSDB; AAS77092.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

Claim 20; SEQ ID No 43264; 103bp; English.

CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridization probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 65 AA;

Query Match Best Local Similarity 2.8%; Score 7; DB 22; Length 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 56 OSLREV 62
Db 39 OSLREV 45

RESULT 68

AAM84103
ID AAM84103 standard; Protein: 73 AA.

XX AAM84103;

DT 07-NOV-2001 (first entry)

DE Human immune/haematopoietic antigen SEQ ID NO:11696.

XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KM cytostatic; gene therapy; vaccine; metastasis.

OS Homo sapiens.

PN WO200157182-A2.

09-AUG-2001.

17-JAN-2001; 2001WO-US01354.

31-JAN-2000; 2000US-0179065.

04-FEB-2000; 2000US-0180628.

24-FEB-2000; 2000US-0184664.

02-MAR-2000; 2000US-0186350.

16-MAR-2000; 2000US-0189874.

17-MAR-2000; 2000US-0190076.

18-APR-2000; 2000US-0198123.

19-MAY-2000; 2000US-0205515.

07-JUN-2000; 2000US-0209467.

28-JUN-2000; 2000US-0214886.

30-JUN-2000; 2000US-0215135.

07-JUL-2000; 2000US-0216647.

11-JUL-2000; 2000US-0217487.

11-JUL-2000; 2000US-0217496.

14-JUL-2000; 2000US-0218290.

26-JUL-2000; 2000US-0220963.

14-AUG-2000; 2000US-0224518.

14-AUG-2000; 2000US-0224519.

14-AUG-2000; 2000US-0225213.

14-AUG-2000; 2000US-0225214.

14-AUG-2000; 2000US-0225266.

14-AUG-2000; 2000US-0225267.

14-AUG-2000; 2000US-0225268.

14-AUG-2000; 2000US-0225270.

14-AUG-2000; 2000US-0225447.

14-AUG-2000; 2000US-0225757.

14-AUG-2000; 2000US-0225758.

14-AUG-2000; 2000US-0225759.

18-AUG-2000; 2000US-0226279.

22-AUG-2000; 2000US-0226681.

22-AUG-2000; 2000US-0226688.

23-AUG-2000; 2000US-0227182.

30-AUG-2000; 2000US-0227009.

01-SEP-2000; 2000US-0228924.

01-SEP-2000; 2000US-0229287.

01-SEP-2000; 2000US-0229343.

01-SEP-2000; 2000US-0229345.

05-SEP-2000; 2000US-0229509.

05-SEP-2000; 2000US-0229513.

06-SEP-2000; 2000US-0230437.

06-SEP-2000; 2000US-0230438.

08-SEP-2000; 2000US-0231242.

08-SEP-2000; 2000US-0231243.

08-SEP-2000; 2000US-0231244.

08-SEP-2000; 2000US-0231413.

08-SEP-2000; 2000US-0231414.

08-SEP-2000; 2000US-0232080.

08-SEP-2000; 2000US-0232081.

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PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234227.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.

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PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251990.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Rosen CA, Barash SC, Ruben SM;
XX
XX DR WPI; 2001-483426/52.
XX
XX DR N-PSDB; AAK56884.
XX
XX PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
XX
XX PS Claim 11; SEQ ID NO 11696; 3071bp + Sequence Listing; English.
XX
XX CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
XX amino acid sequences given in AAM82170 to AAM91921. (I) have cytosolic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patient's own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting
XX the nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/haematopoietic-related diseases, especially
XX cancers and cancer metastases of haematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/haematopoietic antigen genomic
XX sequences from the present invention. AAK51942 to AAK54350 and AAM82169
XX represent sequences used in the exemplification of the present invention.
XX
XX SQ Sequence 73 AA:
XX
XX Query Match 2.8%; Score 7; DB 22; Length 73;
XX Best Local Similarity 100.0%; Pred. No. 70;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 141 ALRRGRG 147
XX |||||
XX Db 65 ALRRGRG 71
XX
XX RESULT 69
XX AAB18724
XX ID AAB18724 standard; Protein: 78 AA.
XX
XX AC AAB18724;
XX
XX XX 22-JAN-2001 (first entry)
XX
XX DE A dermaseptin precursor polypeptide.
XX
XX XX
XX XX Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant;
XX cationic peptide; pathogen resistance.
XX
XX OS Phyllomedusa bicolor.
XX
XX XX
XX XX WO200055337-A1.
XX
XX XX 21-SEP-2000.
XX
XX PD

```

XX 16-MAR-2000; 2000WO-CA00288.
XX
XX 17-MAR-1999; 99US-0125072.
XX
XX (UVVI-) UNIV VICTORIA INNOVATION & DEV CORP.
XX
XX Miera S, Kay WD.
XX
XX WPI; 2000-647077/62.
XX
XX N-PSDB; AAA75749.
XX
XX Transgenic plants resistant to broad spectrum of pathogens useful for
XX producing biologically active cationic peptides, comprises nucleic acid
XX molecule encoding temporin and/or dermaseptin peptides -
XX
XX PS Disclosure; Page 47; 58pp; English.
XX
XX The present sequence represents a dermaseptin precursor polypeptide.
XX The precursor is processed to produce two mature forms, dermaseptin b
XX (AAB18725) and dermaseptin B (AAB18726). Dermaseptin has antibacterial
XX activity, and inhibits fungal growth. Cationic peptides derived from
XX temporins and dermaseptins are used to produce transgenic plants. The
XX transgenic plants are useful for producing biologically active cationic
XX peptides such as temporins and dermaseptins in large quantities. The
XX peptide confers broad spectrum pathogen resistance including enhanced
XX resistance to both fungal and bacterial pathogens in the transgenic
XX plants. The transgenic plants may be used in conventional agricultural
XX applications such as food crops, medical and other applications.
XX
XX SQ Sequence 78 AA;
XX
XX Query Match 2.8%; Score 7; DB 21; Length 78;
XX Best Local Similarity 100.0%; Pred. No. 74;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 37 AALGAVA 43
XX |||||
XX Db 64 AALGAVA 70
XX
XX RESULT 70
XX AAB64816
XX ID AAB64816 standard; Protein; 79 AA.
XX
XX AC AAB64816;
XX
XX 23-MAR-2001 (first entry)
XX
XX Human secreted protein sequence encoded by gene 44 SEQ ID NO:102.
XX
XX Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;
XX antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
XX neurotropic; neuroprotective; antibacterial; vitucide; fungicide;
XX ophthalmological; autoimmune disease; hyperproliferative disorder;
XX cardiovascular disorder; cerebrovascular disorder; infection; chemotaxis;
XX nervous system disorder; ocular disorder; skin aging; wound healing;
XX food additive; tissue regeneration.
XX
XX OS Homo sapiens.
XX
XX PN WO200077256-A1.
XX
XX PD 21-DEC-2000.
XX
XX PF 01-JUN-2000; 2000WO-US14963.
XX
XX PR 11-JUN-1999; 99US-0138631.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX PA
XX
XX PI Rosen CA, Ruben SM, Komatsoulis GA;
XX

DR WPI; 2001-032315/04.
XX
XX N-PSDB; AAF33138.
XX
XX PT Isolated nucleic acid molecule encoding a human secreted protein is
XX used in preventing, treating or ameliorating a medical condition -
XX
XX PS Claim 11; Page 472; 506pp; English.
XX
XX Polynucleotide sequences AAF33095 - AAF33142 encode human secreted
XX proteins AAB64773 - AAB64820. Fragments of the secreted proteins and
XX amino acid sequences which share homology with the fragments are
XX represented in AAB64821 - AAB64880. The genes and proteins have
XX activities dependent on the tissues and cells in which they are
XX expressed. Examples of their activities and the activities of their
XX agonists and antagonists include; immunosuppressive; antiarthritic;
XX antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
XX cerebroprotective; neurotropic; neuroprotective; antibacterial; vitucide;
XX fungicide; and ophthalmological. The secreted proteins, polynucleotides,
XX antagonists and agonists may be useful in treating, preventing and
XX diagnosing diseases and disorders such as autoimmune diseases e.g.
XX rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the
XX breast or liver, cardiovascular disorders e.g. cardiac arrest.
XX cerebrovascular disorders e.g. cerebral ischemia, angiogenesis, nervous
XX system disorders e.g. Alzheimer's disease, infections caused by bacteria,
XX viruses and fungi and ocular disorders e.g. corneal infection. The
XX polypeptides can also be used to aid wound healing and epithelial cell
XX proliferation, to prevent skin aging due to sunburn, to maintain organs
XX before transplantation, for supporting cell culture of primary tissues,
XX to regenerate tissues and in chemotaxis. The polypeptides can also be
XX used as a food additive or preservative to increase or decrease storage
XX capabilities. Included in the invention are sequences AAB64772 and
XX CC AAF33095 - AAF33142 which are used in the isolation and characterisation
XX of the nucleotide and protein sequences of the invention.
XX
XX SQ Sequence 79 AA;
XX
XX Query Match 2.8%; Score 7; DB 22; Length 79;
XX Best Local Similarity 100.0%; Pred. No. 75;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 209 NSCYSAG 215
XX |||||
XX Db 36 NSCYSAG 42
XX
XX RESULT 71
XX AAM89786
XX ID AAM89786 standard; Protein; 83 AA.
XX
XX AC AAM89786;
XX
XX DT 07-NOV-2001 (first entry)
XX
XX DE Human immune/haematopoietic antigen SEQ ID NO:17379.
XX
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis.
XX
XX OS Homo sapiens.
XX
XX PN WO200157182-A2.
XX
XX PD 09-AUG-2001.
XX
XX PF 17-JAN-2001; 2001WO-US01354.
XX
XX PR 31-JAN-2000; 2000US-0179065.
XX
XX PR 04-FEB-2000; 2000US-0180628.
XX
XX PR 24-FEB-2000; 2000US-0184664.
XX
XX PR 02-MAR-2000; 2000US-0186350.
XX
XX PR 16-MAR-2000; 2000US-0189874.
XX
XX PR 17-MAR-2000; 2000US-0190076.
XX
XX PR 18-APR-2000; 2000US-0198123.
XX

PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214885.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
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PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0233968.
PR 14-SEP-2000; 2000US-0233997.
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PR 14-SEP-2000; 2000US-0234063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
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PR 25-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
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PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
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PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
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PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246475.
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PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
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PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
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PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
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PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249267.
PR 17-NOV-2000; 2000US-0249289.
PR 17-NOV-2000; 2000US-0249289.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0251719.
PR 06-DEC-2000; 2000US-0251719.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
(HUMA-) HUMAN GENOME SCI INC.
XX PA
XX (HUMA-) HUMAN GENOME SCI INC.
XX PI
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX DR
XX N-PSDB; AAK62567.
XX PT
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
XX PS
XX Claim 11; SEQ ID NO 17379; 3071pp + Sequence Listing; English.
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
XX amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
CC CC

CC proteins*and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (1) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (1) by expressing inactive proteins or to
 CC supplement the patient's own production of (1). Additionally, (1)
 CC polynucleotides may be used to produce the secreted (1), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (1) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK87654 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention.

SO Sequence 83 AA;

Query Match 2.8%; Score 7; DB 22; Length 83;
 Best Local Similarity 100.0%; Pred. No. 78;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

5 SPFLAP 11
 |||||
 11 SPFLAP 17

Db 11 SPFLAP 17

RESULT 72

AAU44493
 ID AAU44493 standard; Protein; 87 AA.

AC AAU44493;

DT 27-FEB-2002 (first entry)

XX Propionibacterium acnes immunogenic protein #5189.

KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.

OS Propionibacterium acnes.

PN WO200181581-A2.

PD 01-NOV-2001.

XX 20-APR-2001; 2001WO-US12865.

PR 21-APR-2000; 2000US-199047P.

PR 02-JUN-2000; 2000US-208841P.

PR 07-JUL-2000; 2000US-216747P.

XX (CORI-) CORIXA CORP.

PI Skeiky YAM, Pereing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

DR WPI; 2001-616774/71.

DR N-PSDB; AAS59522.

XX Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris -

XX Example 1; SEQ ID No 5688, 1069pp; English.

CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central

CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA).
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 87 AA;

Query Match 2.8%; Score 7; DB 22; Length 87;
 Best Local Similarity 100.0%; Pred. No. 81;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 101 RKRRAVL 107
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 Db 27 RKRRAVL 33

Db 27 RKRRAVL 33

RESULT 73

AAW82267
 ID AAW82267 standard; Protein; 96 AA.

AC AAW82267;

DT 18-FEB-1999 (first entry)

XX Human NTN-2 protein fragment.

KW NTN-2; tumour necrosis factor; TNF; human; diagnosis; screening;
 KW immunogen; gene therapy; modulator; biopharmaceutical industry;
 KW cell growth; cell differentiation; cell function.

OS Homo sapiens.

PN Key Location/Qualifiers
 FT 1..96
 FT Protein /label= NTN-2
 FT /note= "Partial sequence, no start codon given"

FT MISC-difference 26 /label= unknown

XX WO9855620-A1.

PN 10-DEC-1998.

XX 03-JUN-1998; 98WO-US11153.

XX 21-NOV-1997; 97US-0066386.

PR 06-JUN-1997; 97US-0048776.

XX (REGG-) REGENERON PHARM INC.

PI Maslakowski P, Valenzuela D;

DR WPI; 1999-045793/04.

DR N-PSDB; AAV73306.

XX Newly isolated nucleotide encoding human NTN-2 - useful in methods
 PT of diagnosis and in the treatment of the human or animal body

XX Example 1; Page 14; 26pp; English.

CC This sequence represents a fragment of the human tumour necrosis factor
 CC (TNF) homologue, NTN-2. This polypeptide and antibodies generated
 CC from the polypeptide form compositions that are useful in diagnosis (e.g.

```

CC genetic hybridization screens for human NTN-2 transcripts), gene therapy
CC (to modulate human NTN-2 gene expression) and the biopharmaceutical
CC industry (e.g. reagents for screening chemical libraries for suitable
CC pharmaceutical agents). The polypeptides are also useful as immunogens,
CC targets in screening assays, and bioactive reagents for modulating cell
CC growth, differentiation and/or function. The nucleotides are useful as
CC translatable transcripts, hybridization probes, PCR primers, diagnostic
CC nucleotides, and as agents in detecting human NTN-2 genes/transcripts
CC (including variants).
CC
XX Sequence 96 AA;
SQ
Query Match 2.8%; Score 7; DB 20; Length 96;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 209 NSCYSAG 215
Db 54 NSCYSAG 60
|||||
SUIT 74
AAW82269
ID AAW82269 standard; Protein; 96 AA.
AC AAW82269;
XX 18-FEB-1999 (first entry)
DT
XX Human NTN-2 partial protein sequence.
DE
XX NTN-2; tumour necrosis factor; TNF; human; diagnosis; screening;
KW immunogen; gene therapy; modulator; biopharmaceutical industry;
KW cell growth; cell differentiation; cell function.
XX
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH 1..96
FT /label= NTN-2
FT /note= "Partial sequence, no start codon given"
FT Misc-difference 26
FT /label= unknown
PN
XX W09855621-A1.
PD 10-DEC-1998.
XX 03-JUN-1998; 98WO-US11294.
PR 21-NOV-1997; 97US-0066387.
PR 06-JUN-1997; 97US-0048776.
XX (REGC-) REGENERON PHARM INC.
PA
XX Maslakowski P, Valenzuela D;
PI
XX WPI: 1999-045794/04.
DR N-PSDB; AAV73308.
XX
XX Newly isolated nucleotide encoding human NTN-2 - useful in methods
PT of diagnosis and in the treatment of the human or animal body
XX
XX Example 1; Page 14; 26pp; English.
XX
XX This sequence encodes a fragment of the human tumour necrosis factor
CC (TNF) homologue, NTN-2. This polypeptide and antibodies generated
CC from the polypeptide form compositions that are useful in diagnosis (e.g.
CC genetic hybridization screens for human NTN-2 transcripts), gene therapy
CC (to modulate human NTN-2 gene expression) and the biopharmaceutical
CC industry (e.g. reagents for screening chemical libraries for suitable
CC pharmaceutical agents). The polypeptides are also useful as immunogens,
CC targets in screening assays, and bioactive reagents for modulating cell

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CC growth, differentiation and/or function. The nucleotides are useful as
CC translatable transcripts, hybridization probes, PCR primers, diagnostic
CC nucleotides, and as agents in detecting human NTN-2 genes/transcripts
CC (including variants).
CC
XX Sequence 96 AA;
SQ
Query Match 2.8%; Score 7; DB 20; Length 96;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 209 NSCYSAG 215
Db 54 NSCYSAG 60
|||||
RESULT 75
AAO08276
ID AAO08276 standard; Protein; 105 AA.
XX
XX AAO08276;
XX 06-NOV-2001 (first entry)
DT
XX Human polypeptide SEQ ID NO 22168.
DE
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
XX Homo sapiens.
OS
XX W0200164835-A2.
PN
XX 07-SEP-2001.
PD
XX 26-FEB-2001; 2001WO-US04927.
PF
XX 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
XX
XX (HXSE-) HXSEQ INC.
PA
XX Tang YT, Liu C, Drmanac RT;
PI
XX WPI: 2001-514838/56.
DR N-PSDB; AAI86207.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
XX Claim 20; SEQ ID NO 22168; 1399pp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 105 AA;
SQ
Query Match 2.8%; Score 7; DB 22; Length 105;

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Best Local Similarity 100.0%; Pred. No. 96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 LAPKGP 15
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Db 87 LAPKGP 93

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Job time : 40 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 07:31:11 ; Search time 75 Seconds

(without alignments)
444.169 Million cell updates/sec

Title: US-09-724-341-8

Perfect score: 1304
Sequence: 1 MPASSPFLAPKGPNGMG.....RAKAKNLSPHGFLEFVKL 250

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

a1 number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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SUMMARIES

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3	1304	100.0	250	20	AAV04283
4	1304	100.0	250	20	AAW83368
5	1304	100.0	250	21	AAV93692
6	1304	100.0	250	21	AAV01323
7	1304	100.0	250	22	AAV09243
8	1304	100.0	250	22	AAV52329
9	1304	100.0	250	22	AAV11981
10	1304	100.0	250	23	AAV99305

11	1304	100.0	250	23	ABE81486	Human ZTNF2 amino
12	1304	100.0	250	23	ABP47228	Human BLYS binding
13	1304	100.0	250	23	AAU79155	Human APRIL (a pro
14	1299	99.6	250	20	AAW93588	Human TNFR1-beta p
15	1299	99.6	250	21	AAV95670	Human death recept
16	1299	99.6	250	23	AAE15502	Human APRIL G70 pr
17	1299	99.6	250	20	AAE05442	Human normal bladd
18	1297	99.6	250	21	AAE54342	Human pancreatic c
19	1296	99.4	250	20	AAV05745	Tumour necrosis fa
20	1296	99.4	250	23	AAU99510	Human tumour necro
21	1296	99.4	250	23	AAU5406	Tumour necrosis fa
22	1290	98.9	248	23	AAE15482	Human APRIL G70 pr
23	1285	98.5	247	20	AAE128836	Human TNF-related
24	1285	98.5	247	22	AAE62327	Human TRDL-1gamma
25	1241	95.2	248	22	AAE07877	Human APRIL protei
26	1206	92.5	233	20	AAV09551	Human TRAILK-3 pr
27	1203	92.3	233	23	AAU99508	Human tumour necro
28	1203	92.3	233	23	AAU75402	Tumour necrosis fa
29	1200	92.0	234	22	AAE62330	Human TRDL-1beta p
30	1199	91.9	233	18	AAW37002	Human tumour necro
31	1195	91.6	234	20	AAV28835	Human TNF-related
32	1195	91.6	244	20	AAV74026	Human prostate tum
33	1187	91.0	234	23	AAU75407	Human tumour necro
34	1187	91.0	234	23	AAU75407	Tumour necrosis fa
35	1053	80.8	205	20	AAE12225	Human TNF2 protei
36	1013.5	77.7	240	20	AAE15483	Mouse APRIL-beta p
37	1006	77.1	240	23	AAE15483	Mouse APRIL/G70 pr
38	978.5	75.0	232	21	AAV79672	Mouse death recept
39	967.5	74.2	232	20	AAV04284	Mouse APRIL protei
40	967.5	74.2	232	22	AAE07878	Mouse APRIL protei
41	858	65.8	168	18	AAW37003	Human tumour necro
42	858	65.8	168	23	AAU99509	Human tumour necro
43	858	65.8	168	23	AAU75403	Tumour necrosis fa
44	762	58.4	147	20	AAW88369	Tumour necrosis fa
45	759	58.2	177	23	AAO14134	Protein of a FLAG

ALIGNMENTS

RESULT 1	AAV06485	standard; Protein; 250 AA.
ID	AAV06485	
AC	AAV06485;	
XX	27-SEP-1999	(first entry)
DT	27-SEP-1999	
XX		
DE	Human tumour-associated protein PRO715.	
XX		
KM	PRO715; UNQ383; cancer; tumour necrosis family; diagnosis; therapy;	
KW	human.	
XX		
OS	Homo sapiens.	
XX		
PN	WO9935170-A2.	
XX		
PD	15-JUL-1999.	
XX		
PF	05-JAN-1999;	99WO-US00106.
XX		
PR	20-NOV-1998;	98US-0109304.
PR	05-JAN-1998;	98US-0070440.
PR	26-APR-1998;	98US-0083500.
PR	22-MAY-1998;	98US-0086414.
PR	10-JUN-1998;	98US-0088742.
PR	10-NOV-1998;	98US-0107783.
XX		
PA	(GETH) GENENTECH INC.	
XX		
PI	Botstein D, Goddard A, Gurney AL, Hillen KJ, Lawrence DA;	
PI	Roy WA, Wood WI;	
XX		

DR WPI; 1999-430385/36.
DR N-PSDB; AAX87262.

PT Antibody against proteins expressed in neoplastic cells, useful for
PT tumour diagnosis and treatment

PS Example 1, Fig 18; 162pp; English.

XX This sequence represents human PRO715 (UNQ382), a protein encoded
CC by the novel cDNA clone DNA52722 (see AAX87262) that shows homology
CC to members of the tumour necrosis factor family. Amplification of
CC DNA52722 was observed in various colon and lung tumors and cell
CC lines, suggesting a role in tumour formation or growth. Antagonists
CC (e.g. antibodies) directed to PRO715 may have use in cancer therapy.
CC The invention identifies 14 genes (see AAX87254-67) that are amplified
CC in the genome of tumour cells. Such amplification is expected to be
CC associated with overexpression of the gene product and to contribute
CC to tumorigenesis. The encoded proteins (see AAY06477-90) may be
CC useful targets for the diagnosis and/or treatment (including
CC prevention) of certain cancers, and may act as predictors of the
CC prognosis of tumour treatment. Antibodies that bind the proteins
XX are claimed and used in claimed cancer diagnostic kits.

XX Sequence 250 AA;

Query Match 100.0%; Score 1304; DB 20; Length 250;
Best Local Similarity 100.0%; Pred. No. 4,1e-127;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPASSPFLAPKGPNNNGGVPREBPAISVALWLSWGAALGAVACAMALLTQOTELQSLRR 60

DB 1 MPASSPFLAPKGPNNNGGVPREBPAISVALWLSWGAALGAVACAMALLTQOTELQSLRR 60

QY 61 EVSRLOGTGSPQNGEGYPMQSLPEQSSDALEAMENGRSRRAVLTKQKQHSVLHL 120

DB 61 EVSRLOGTGSPQNGEGYPMQSLPEQSSDALEAMENGRSRRAVLTKQKQHSVLHL 120

QY 121 VPINATSKDDSDVTEVMQPALRRGRGLQAGYGVRIQDAGVLLYSQVLFQDVTFTMGQ 180

DB 121 VPINATSKDDSDVTEVMQPALRRGRGLQAGYGVRIQDAGVLLYSQVLFQDVTFTMGQ 180

QY 181 VVSREGQGRQETLFRICRISMPSPHPRAYNSCYAGVFLHOGDILSVIIPRAAKLNLS 240

DB 181 VVSREGQGRQETLFRICRISMPSPHPRAYNSCYAGVFLHOGDILSVIIPRAAKLNLS 240

QY 241 HGTFLGFPVKL 250

DB 241 HGTFLGFPVKL 250

RESULT 2

ID AAY17832 standard; Protein; 250 AA.

AC AAY17832;

DT 12-AUG-1999 (first entry)

DE Human PRO715 protein sequence.

KW Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
KW secreted protein; transmembrane protein; inflammation disorder.

XX Homo sapiens.

XX WO9928462-A2.

XX 10-JUN-1999.

XX 01-DEC-1998; 98WO-US25108.

XX 25-FEB-1998; 98US-0075945.

PR 03-DEC-1997; 97US-0067411.

PR 11-DEC-1997; 97US-0069278.

PR 11-DEC-1997; 97US-0069334.

PR 11-DEC-1997; 97US-0069335.

PR 12-DEC-1997; 97US-0069425.

PR 16-DEC-1997; 97US-0069694.

PR 16-DEC-1997; 97US-0069696.

PR 16-DEC-1997; 97US-0069702.

PR 17-DEC-1997; 97US-0069870.

PR 17-DEC-1997; 97US-0069873.

PR 18-DEC-1997; 97US-0068017.

PR 05-JAN-1998; 98US-0070440.

PR 09-FEB-1998; 98US-0074086.

PR 09-FEB-1998; 98US-0074092.

XX (GENTH) GENENTECH INC.

PI Baker KP, Chen J, Goddard A, Gurney AL, Wood WI;

PI yvan J;

XX WPI; 1999-371118/31.

DR N-PSDB; AAX80057.

XX Nucleic acids encoding PRO secreted and transmembrane proteins

PS Claim 12; Fig 31; 123pp; English.

XX The present invention describes nucleic acids encoding PRO secreted and

CC transmembrane proteins used therapeutically. The PRO proteins have

CC cytosolic, anti-inflammatory, anti-proliferative and immunosuppressive

CC activity. The proteins and polynucleotides can be used in therapy,

CC identification of homologues, raising antibodies and design of probes

CC and primers. They can be used in a range of diseases related to proteins

CC that they have homology with, e.g. a PRO protein having homology to

CC complement proteins may be used in inflammatory responses.

XX Sequence 250 AA;

QY Query Match 100.0%; Score 1304; DB 20; Length 250;

Best Local Similarity 100.0%; Pred. No. 4,1e-127;

Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPASSPFLAPKGPNNNGGVPREBPAISVALWLSWGAALGAVACAMALLTQOTELQSLRR 60

DB 1 MPASSPFLAPKGPNNNGGVPREBPAISVALWLSWGAALGAVACAMALLTQOTELQSLRR 60

QY 61 EVSRLOGTGSPQNGEGYPMQSLPEQSSDALEAMENGRSRRAVLTKQKQHSVLHL 120

DB 61 EVSRLOGTGSPQNGEGYPMQSLPEQSSDALEAMENGRSRRAVLTKQKQHSVLHL 120

QY 121 VPINATSKDDSDVTEVMQPALRRGRGLQAGYGVRIQDAGVLLYSQVLFQDVTFTMGQ 180

DB 121 VPINATSKDDSDVTEVMQPALRRGRGLQAGYGVRIQDAGVLLYSQVLFQDVTFTMGQ 180

QY 181 VVSREGQGRQETLFRICRISMPSPHPRAYNSCYAGVFLHOGDILSVIIPRAAKLNLS 240

DB 181 VVSREGQGRQETLFRICRISMPSPHPRAYNSCYAGVFLHOGDILSVIIPRAAKLNLS 240

QY 241 HGTFLGFPVKL 250

DB 241 HGTFLGFPVKL 250

RESULT 3

ID AAY04283 standard; Protein; 250 AA.

AC AAY04283;

DT 17-JUN-1999 (first entry)

DE Human APRIL protein sequence.

KW Human APRIL protein sequence; TNF; proliferating inducing agent;

KM immune disorder; cancer.

OS Homo sapiens.

PN WO9912965-A2.

XX 18-MAR-1999.

XX 11-SEP-1998; 98WO-US19191.

XX 26-MAR-1998; 98US-0079384.

PR 12-SEP-1997; 97US-0058786.

XX (BIO) BIOGEN INC.

XX (BIO) BIOGEN INC.

XX WPI; 1999-215028/18.

DR N-PSDB; AAX30124.

PT A Proliferating Inducing Agent (APRIL), a member of the Tumour

XX Necrosis Factor Family - useful as diagnostic agents and for

XX prevention or treatment of immune disorders and cancer

XX Claim 12; Page 46; 47pp; English.

XX The present sequence represents a proliferating inducing agent (APRIL)

XX isolated from human. APRIL is a member of the tumour necrosis factor

XX family, and essentially free of normally associated proteins. APRIL and

XX APRIL antibodies are useful in pharmaceutical compositions for

XX preventing or reducing severity of an autoimmune disease or an immune

XX response to tissue graft. The composition is also useful for stimulating

XX or suppressing the immune system, and treating cancer. APRIL is also

XX useful for treating APRIL-related disorders by delivering via a vector

XX (preferably viral vector) (gene therapy) into a mammalian (preferably

XX human) cell. Labeled APRIL and fragments are useful for identifying

XX APRIL receptors by screening compositions. Antisense DNA and antibodies

XX and modified APRIL (preferably an anti-APRIL receptor antibody) are

XX useful as blocking agents for inducing cell death by interfering with

XX APRIL receptors. The blocking agent is preferably administered with

XX interferon- γ and treats, suppresses or alters an immune response

XX involving a signalling pathway between APRIL and its receptor

XX (preferably involving human carcinoma cells); and also treats,

XX suppresses or alters the progression of cancer (preferably at least one

XX chemotherapeutic agent is also administered, and radiation therapy is

XX also given to the patient.

XX Sequence 250 AA;

Query Match 100.0%; Score 1304; DB 20; Length 250;

Best Local Similarity 100.0%; Pred. No. 4.1e-127; Mismatches 0; Indels 0; Gaps 0;

Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPASSPFLAARPGPNNGGVRREPALSVALWLSGALGAVACAMALLTOOTELQSLRR 60

DB 1 MPASSPFLAARPGPNNGGVRREPALSVALWLSGALGAVACAMALLTOOTELQSLRR 60

QY 61 EVSLQGTGGSGONGEGVPWQSLPEQSSDALAEWNGERSRKRRAVLTQKKKHSHVHL 120

DB 61 EVSLQGTGGSGONGEGVPWQSLPEQSSDALAEWNGERSRKRRAVLTQKKKHSHVHL 120

QY 121 VPINATSKDSDVTEVMMQALRRGRLQAGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180

DB 121 VPINATSKDSDVTEVMMQALRRGRLQAGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180

QY 181 VVSREGGROETTLFRCLIRSMPSHPRAYNSCYAGVFLHOGDILSVIIPARAKNLSP 240

DB 181 VVSREGGROETTLFRCLIRSMPSHPRAYNSCYAGVFLHOGDILSVIIPARAKNLSP 240

QY 241 HGTFLGFVKL 250

DB 241 HGTFLGFVKL 250

RESULT 4

ID AAW88368 standard; Protein; 250 AA.

XX AAW88368;

XX 26-APR-1999 (first entry).

XX Tumour necrosis factor-gamma.

XX Tumour necrosis factor-gamma; TNF-gamma; human; inflammation;

XX cancer; tumour; metastasis; graft versus host disease;

XX drug screening; therapy; diagnosis.

XX Homo sapiens.

XX WO9900518-A1.

XX 07-JAN-1999.

XX 12-JUN-1998; 98WO-US12101.

XX 26-JUN-1997; 97US-0883086.

XX (ABBO) ABBOTT LAB.

XX WPI; 1999-095761/08.

DR N-PSDB; AAX06771.

PT Tumour necrosis factor gamma detecte target polynucleotides - useful

PT for, e.g. treating inflammation, cancer and graft versus host

XX Claim 16; Page 84-85; 106pp; English.

XX This is the amino acid sequence of human tumour necrosis factor

XX gamma (TNFG), a novel member of the TNF family of ligands. The

XX invention provides a method of producing TNFG polypeptide using

XX a recombinant expressing system comprising a nucleic acid sequence

XX (see AAX06771) encoding TNFG and transformed host cells. Also

XX provided are a procedure of producing biologically active soluble

XX TNFG (see AAW88369), which can be used to treat deficiencies of TNFG

XX and disease conditions ameliorated by TNFG. Antibodies,

XX antagonists and inhibitors of such a polypeptide may be used to

XX treat TNFG-associated diseases, tumours or metastases, and to

XX screen for, diagnose and monitor conditions attributable to TNFG,

XX especially inflammation, cancer and graft versus host disease.

XX Cells expressing TNFG on their surface can be used to screen for

XX (ant)agonists, and to detect receptor binding.

XX Sequence 250 AA;

Query Match 100.0%; Score 1304; DB 20; Length 250;

Best Local Similarity 100.0%; Pred. No. 4.1e-127; Mismatches 0; Indels 0; Gaps 0;

Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPASSPFLAARPGPNNGGVRREPALSVALWLSGALGAVACAMALLTOOTELQSLRR 60

DB 1 MPASSPFLAARPGPNNGGVRREPALSVALWLSGALGAVACAMALLTOOTELQSLRR 60

QY 61 EVSLQGTGGSGONGEGVPWQSLPEQSSDALAEWNGERSRKRRAVLTQKKKHSHVHL 120

DB 61 EVSLQGTGGSGONGEGVPWQSLPEQSSDALAEWNGERSRKRRAVLTQKKKHSHVHL 120

QY 121 VPINATSKDSDVTEVMMQALRRGRLQAGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180

DB 121 VPINATSKDSDVTEVMMQALRRGRLQAGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ 180

QY 181 VVSREGGROETTLFRCLIRSMPSHPRAYNSCYAGVFLHOGDILSVIIPARAKNLSP 240

DB 181 VVSREGGROETTLFRCLIRSMPSHPRAYNSCYAGVFLHOGDILSVIIPARAKNLSP 240

Db 181 VSRGEGROETLPRCIRSMPSHPDRAYNSCYSAGVPHLHGDIILSVIIPRAKLNLSLP 240
 QY 241 HGTFLGFVKL 250
 Db 241 HGTFLGFVKL 250

RESULT 5

AAV93692 standard; Protein: 250 AA.

AAV93692;

03-OCT-2000 (first entry)

Amino acid sequence of novel polypeptide PRO715.

PRO201; PRO392; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357;
 KM PRO715; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell;
 tumourigenesis; cancer; neoplastic cell growth; cell proliferation.

Homo sapiens.

Key Location/Qualifiers

Peptide 1..40

/note= "signal sequence"

Region 34..45

/note= "prokaryotic membrane lipoprotein attachment site"

Modified-site 36..42

/note= "N-myristoylation site"

Modified-site 40..46

/note= "N-myristoylation site"

Modified-site 124..128

/note= "N-glycosylation site"

Modified-site 156..164

/note= "tyrosine kinase phosphorylation site"

Modified-site 179..185

/note= "N-myristoylation site"

Modified-site 242..248

/note= "N-myristoylation site"

WO200037640-A2.

29-JUN-2000.

16-DEC-1999; 99WO-US10095.

22-DEC-1998; 98US-0113296.

08-MAR-1999; 99WO-US05028.

02-JUN-1999; 99WO-US12252.

01-SEP-1999; 99WO-US20111.

15-SEP-1999; 99WO-US21030.

30-NOV-1999; 99WO-US28313.

30-NOV-1999; 99WO-US28409.

01-DEC-1999; 99WO-US28301.

02-DEC-1999; 99WO-US28565.

(GETH) GENENTECH INC.

Botstein D, Goddard A, Gurney AL, Hillan K, Lawrence DA, Roy MA,

Wood WI;

WPI: 2000-452188/39.

N-PSDB; AAA46928.

New anti-polypeptide antibody useful in the treatment and diagnosis of

neoplastic cell growth and proliferation -

Claim 61; Fig 18; 220pp; English.

The present sequence represents a novel human polypeptide. The

specification describes novel polypeptides designated PRO201, PRO392,

PRO327, PRO1265, PRO344, PRO343, PRO347, PRO357, PRO1017,

CC

CC PRO112, PRO509, PRO853 and PRO882. These genes are amplified in
 CC the genome of tumour cells. The polypeptides are believed to contribute
 CC to tumourigenesis. The polypeptides are useful target for the
 CC identification of certain cancers, and may act as predictors of the
 CC prognosis of tumour treatment. Antibodies against these polypeptides
 CC are useful in the treatment and diagnosis of neoplastic cell growth
 CC and proliferation in mammals.

Sequence 250 AA;

Query Match 100.0%; Score 1304; DB 21; Length 250;

Best Local Similarity 100.0%; Pred. No. 4, 1e-127; Mismatches 0; Gaps 0;

Matches 250; Conservative 0; Indels 0;

1 MPASSPFLAPKGPFGPMGVPREPALSVLWLSWGAALGAVACAMALLTOETELSLRR 60

1 MPASSPFLAPKGPFGPMGVPREPALSVLWLSWGAALGAVACAMALLTOETELSLRR 60

61 EVSRLOGTGSPQNGEGYPMQSLPEQSSDALWENGERSRKRAVLTQKQKSHVHL 120

61 EVSRLOGTGSPQNGEGYPMQSLPEQSSDALWENGERSRKRAVLTQKQKSHVHL 120

121 VPINATSKDSDVTEVWMOALRRGRGLQAGYGVRIQDAGVVLVSQVLFQDVTFTMGQ 180

121 VPINATSKDSDVTEVWMOALRRGRGLQAGYGVRIQDAGVVLVSQVLFQDVTFTMGQ 180

181 VSRGEGROETLPRCIRSMPSHPDRAYNSCYSAGVPHLHGDIILSVIIPRAKLNLSLP 240

181 VSRGEGROETLPRCIRSMPSHPDRAYNSCYSAGVPHLHGDIILSVIIPRAKLNLSLP 240

241 HGTFLGFVKL 250

241 HGTFLGFVKL 250

241 HGTFLGFVKL 250

241 HGTFLGFVKL 250

241 HGTFLGFVKL 250

241 HGTFLGFVKL 250

241 HGTFLGFVKL 250

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241 HGTFLGFVKL 250

241 HGTFLGFVKL 250

241 HGTFLGFVKL 250

241 HGTFLGFVKL 250

241 HGTFLGFVKL 250

241 HGTFLGFVKL 250

PD 08-JUN-2000.
 XX
 PF 01-DEC-1999; 99WO-US28301.
 XX
 PR 01-DEC-1998; 98WO-US25108.
 PR 16-DEC-1998; 98US-0112850.
 PR 22-DEC-1998; 98US-0113296.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
 PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
 PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
 XX
 DR WPI; 2000-412324/35.
 DR N-PSDB; AAA49565.
 XX
 PT New human nucleic acids encoding secreted and transmembrane
 PT polypeptides, designated as PRO polypeptides, useful as pharmaceutical
 PT and diagnostic agents
 XX
 CS Claim 12; Fig 28; 187pp; English.
 XX
 CC New human nucleic acids encoding secreted and transmembrane
 CC polypeptides which are designated as PRO polypeptides are described
 CC The membrane-bound proteins have various industrial applications,
 CC including as pharmaceutical and diagnostic agents. The membrane-bound
 CC proteins can also be employed for screening of potential peptide or
 CC small molecule inhibitors of the relevant receptor/ligand interaction.
 CC Anti-PRO antibodies are useful for the affinity purification of PRO
 CC from recombinant cell culture or natural sources.
 XX
 SQ Sequence 250 AA;
 Query Match 100.0%; Score 1304; DB 21; Length 250;
 Best Local Similarity 100.0%; Pred. No. 4,1e-127;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPASSPFLAPKGPNGMGVREPALSVALLWSGALGAVACAMALLTQOTELQSLRR 60
 DB 1 MPASSPFLAPKGPNGMGVREPALSVALLWSGALGAVACAMALLTQOTELQSLRR 60
 QY 61 EVSRLQGTGSPQNGEGYPMQSLPEQSSDALEAENGERSKRAVLTQKKQHSVHL 120
 DB 61 EVSRLQGTGSPQNGEGYPMQSLPEQSSDALEAENGERSKRAVLTQKKQHSVHL 120
 QY 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYGVRIODAGVLLYSQVLFQDVTFTMGQ 180
 DB 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYGVRIODAGVLLYSQVLFQDVTFTMGQ 180
 QY 181 VVSREGGROETLFRICIRSMPSHPDRAYNSCYSAGVPHLQGDILSVIIPRAAKLNLS 240
 DB 181 VVSREGGROETLFRICIRSMPSHPDRAYNSCYSAGVPHLQGDILSVIIPRAAKLNLS 240
 QY 241 HGTFLGFVKL 250
 DB 241 HGTFLGFVKL 250
 RESULT 7
 ID AAE09243
 ID AAE09243 standard; Protein; 250 AA.
 XX
 AC AAE09243;
 XX
 DT 19-NOV-2001 (first entry)
 XX
 DE Human APRIL protein.
 XX
 KM Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
 KM TNFR; TACT; BCMA; therapy; cancer; leukemia; myeloma; lymphoma;
 KM autoimmune disease; rheumatoid arthritis; multiple sclerosis;
 KM psoriasis.

XX Homo sapiens.
 OS
 XX WO200160397-A1.
 PN
 XX 23-AUG-2001.
 PD
 XX 28-NOV-2000; 2000WO-US32378.
 XX
 PF 16-FEB-2000; 2000US-0182938.
 PR 22-AUG-2000; 2000US-0226986.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Masters SA, Pletti RM;
 PI Yan M;
 XX
 DR WPI; 2001-541628/60.
 DR N-PSDB; AAD15904.
 XX
 PT Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
 PT activity for treating autoimmune disorders and cancer, comprises
 PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
 PT antagonists
 XX
 CS Claim 20; Fig 4; 160pp; English.
 XX
 CC The invention relates to methods of using one or more agonists or
 CC antagonists to modulate the activity of the members of TNF (tumour
 CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)
 CC e.g. TACT or BCMA. The method is useful for treating pathological
 CC conditions or diseases associated with increased TALL-1 and APRIL
 CC expression or activity. TALL-1 and APRIL antagonists are used to
 CC block the interaction between APRIL and TALL-1 with TACT or BCMA.
 CC They are useful for treating a mammal suffering from cancer such
 CC as leukemia, lymphoma, myeloma, cancers of lung and colon and
 CC autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,
 CC psoriasis and lupus erythematosus. The present sequence is human
 CC APRIL protein.
 XX
 SQ Sequence 250 AA;
 Query Match 100.0%; Score 1304; DB 22; Length 250;
 Best Local Similarity 100.0%; Pred. No. 4,1e-127;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPASSPFLAPKGPNGMGVREPALSVALLWSGALGAVACAMALLTQOTELQSLRR 60
 DB 1 MPASSPFLAPKGPNGMGVREPALSVALLWSGALGAVACAMALLTQOTELQSLRR 60
 QY 61 EVSRLQGTGSPQNGEGYPMQSLPEQSSDALEAENGERSKRAVLTQKKQHSVHL 120
 DB 61 EVSRLQGTGSPQNGEGYPMQSLPEQSSDALEAENGERSKRAVLTQKKQHSVHL 120
 QY 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYGVRIODAGVLLYSQVLFQDVTFTMGQ 180
 DB 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYGVRIODAGVLLYSQVLFQDVTFTMGQ 180
 QY 181 VVSREGGROETLFRICIRSMPSHPDRAYNSCYSAGVPHLQGDILSVIIPRAAKLNLS 240
 DB 181 VVSREGGROETLFRICIRSMPSHPDRAYNSCYSAGVPHLQGDILSVIIPRAAKLNLS 240
 QY 241 HGTFLGFVKL 250
 DB 241 HGTFLGFVKL 250
 RESULT 8
 ID AAB62329
 ID AAB62329 standard; protein; 250 AA.
 XX
 AC AAB62329;
 XX

DT 29-JUN-2001 (first entry)
 XX Human TRDL-1alpha polypeptide.
 DE Tumour necrosis factor related death ligand-1gamma; TRDL-1gamma; TRDL;
 XX cell death; apoptosis; human; TRDL-1alpha.
 KW Homo sapiens.
 XX WO200125256-A2.
 FN 12-APR-2001.
 PD 06-OCT-2000; 2000WO-US27868.
 PF 06-OCT-1999; 99US-0157913.
 PR (UTAH) UNIV UTAH RES FOUND.
 PA Jones D, Manos E;
 PI WPI; 2001-281728/29.
 XX Isolated and purified polynucleotide encoding human tumor necrosis
 FT factor related death ligand (TRDL)-1 gamma useful for identifying
 FT agents that inhibit or enhance TRDL-1 gamma mediated induction of
 FT apoptosis -
 XX
 PS Disclosure: Fig 1; 39pp; English.
 XX The invention provides a human tumour necrosis factor related death
 CC ligand-1gamma (TRDL-1gamma). The TRDL-1gamma polypeptide can be
 CC expressed by standard recombinant methodology. TRDL-1gamma stimulates
 CC Jurkat cell death. It is useful for identifying agents capable of
 CC inhibiting or enhancing TRDL-1gamma mediated induction of apoptosis.
 CC The present sequence represents a TRDL-1alpha polypeptide, used in
 CC alignment studies.
 CC
 XX Sequence 250 AA;
 SQ
 Query Match 100.0%; Score 1304; DB 22; Length 250;
 Best Local Similarity 100.0%; Pred. No. 4.1e-127;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPASSPFLAPKGPNGMGPVREPALSVLWLSGALGAVACAMALITQOTELQSLRR 60
 DB 1 MPASSPFLAPKGPNGMGPVREPALSVLWLSGALGAVACAMALITQOTELQSLRR 60
 61 EVSRLQGTGSPQNGEGYVWQSLPEQSSDALFAMWENGERSRRRAVLTKQKKQHSVLHL 120
 61 EVSRLQGTGSPQNGEGYVWQSLPEQSSDALFAMWENGERSRRRAVLTKQKKQHSVLHL 120
 QY 121 VVINTSKDSDVTEVMQPALRGKGLAQGYVRIODAGVLYLSQVLFDQVPTMQQ 180
 DB 121 VVINTSKDSDVTEVMQPALRGKGLAQGYVRIODAGVLYLSQVLFDQVPTMQQ 180
 QY 181 VVREGQGOETLFCIRSPSHPDRAVNSCYSAGVFHLHQDILSVIIPARAKLNLSP 240
 DB 181 VVREGQGOETLFCIRSPSHPDRAVNSCYSAGVFHLHQDILSVIIPARAKLNLSP 240
 QY 241 HGTFLGFKVL 250
 DB 241 HGTFLGFKVL 250
 RESULT 9
 ID AAY71981 standard; Protein; 250 AA.
 AC AAY71981;
 DT 28-MAR-2001 (first entry)

DE Human TNF and Apol-related Leucocyte-expressed ligand 2/APRIL protein.
 XX
 KW Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
 KW Tumour necrosis factor and Apol-related Leucocyte expressed ligand;
 KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
 KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
 KW thrombocytopenia purpura; acute rheumatic fever; myasthenia gravis;
 KW haemolytic anaemia; Grave's disease; Goodpasture's syndrome; TALL2/APRIL;
 KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
 KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Domain
 FT /label= Transmembrane_domain
 FT 116..122
 FT /label= Beta_strand
 FT 138..140
 FT /label= Beta_strand
 FT 148..150
 FT /label= Beta_strand
 FT 153..156
 FT /label= Beta_strand
 FT 162..173
 FT /label= Beta_strand
 FT 187..192
 FT /label= Beta_strand
 FT 201..209
 FT /label= Beta_strand
 FT 210..217
 FT /label= Beta_strand
 FT 222..230
 FT /label= Beta_strand
 FT 243..250
 FT /label= Beta_strand
 XX
 PN WO200068378-A1.
 PD 16-NOV-2000.
 XX
 PF 05-MAY-2000; 2000NO-US12266.
 XX
 PR 06-MAY-1999; 99US-0132892.
 PR 01-MAY-2000; 2000US-0201012.
 XX
 PA (NAJE-) NAT JEWISH MEDICAL & RES CENT.
 XX
 P1 Shu HS;
 XX
 DR WPI; 2001-016094/02.
 XX
 PT Isolated TALL-1 protein is used to identify compounds that regulate B
 PT lymphocyte proliferation, used to treat B lymphocyte associated
 PT autoimmune disorders -
 XX
 PS Example 1; Fig 1a; 112pp; English.
 XX
 CC The present invention relates to Tumour necrosis factor (TNF) and
 CC Apol-related Leucocyte expressed ligand 1 (TALL-1) nucleic acid
 CC molecules, proteins (including homologues), and their antidiodes. The
 CC invention in particular relates to methods for regulating the
 CC interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell
 CC maturation factor) to regulate monocyte, macrophage and B lymphocyte
 CC mediated immune responses. TALL-1 protein is useful for identifying
 CC compounds that regulate B lymphocyte proliferation. It is also useful for
 CC treating B lymphocyte associated autoimmune disorders like Rheumatoid
 CC arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes
 CC mellitus, multiple sclerosis, myasthenia gravis, Grave's disease,
 CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura,
 CC Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever,
 CC post-streptococcal glomerulonephritis, or polyarteritis nodosa.
 CC The TALL-1 protein and its corresponding nucleic acid sequence are also

CC useful in diagnostic assays.
 CC The present sequence is human Tumour necrosis factor (TNF) and
 CC Apol-related leucocyte-expressed ligand 2 (TALL-2/APRIL protein.
 CC TALL-2/APRIL is encoded by the second TNF/FasL like gene. TALL2/APRIL
 CC also belongs to the subfamily of TNF family of ligands.
 XX
 SO Sequence 250 AA:

Query Match 100.0%; Score 1304; DB 22; Length 250;
 Best Local Similarity 100.0%; Pred. No. 4.1e-127;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPASSPFLAPKGPNGGVPREPALSVALLMSGALGAVACAMALLTQOTELQSLRR 60
 DB 1 MPASSPFLAPKGPNGGVPREPALSVALLMSGALGAVACAMALLTQOTELQSLRR 60
 QY 61 EVSRLQGTGSPQNGEGYPMQSLPEQSSDALAEWNGERSRKRRAVLTOKOKHSHVHL 120
 DB 61 EVSRLQGTGSPQNGEGYPMQSLPEQSSDALAEWNGERSRKRRAVLTOKOKHSHVHL 120
 QY 121 VPINATSKDSDVTEVMQPALRRGRLQAGYGVRIQDAGVLLYSQVLFQDVTFTMGQ 180
 DB 121 VPINATSKDSDVTEVMQPALRRGRLQAGYGVRIQDAGVLLYSQVLFQDVTFTMGQ 180
 QY 181 VVSREGQROETLFRCLISMPSHDPRAVNSCYAGVFHLHOGDILSVIIPRAKLNLS 240
 DB 181 VVSREGQROETLFRCLISMPSHDPRAVNSCYAGVFHLHOGDILSVIIPRAKLNLS 240
 QY 241 HGTFLGFVKL 250
 DB 241 HGTFLGFVKL 250

RESULT 10
 ID AAU9305
 AAU9305 standard; Protein: 250 AA.

24-SEP-2002 (first entry)

XX Human tumour necrosis factor ligand (TNFL), TRASH protein #1.
 DE Human tumour necrosis factor ligand (TNFL), TRASH protein #1.
 KW Human; anti-inflammatory; immunomodulatory; TRASH; TNFL; TANGO 118;
 KW tumour necrosis factor ligand; signal transduction; gene therapy;
 KW diagnosis; immune response; inflammatory disorder;
 KW differential disorder; developmental disorder.

Homo sapiens.

XX Key Location/Qualifiers
 FT 1..44
 FT /note= "N-terminal signal transmembrane anchor
 FT specifically claimed in claim 27 of the
 FT specification"
 FT Region 18..250
 FT /note= "This region, TRASH protein #2, is specifically
 FT claimed in claim 28 of the specification"
 FT Region 46..250
 FT /note= "This region, TRASH protein #3, is specifically
 FT claimed in claim 28 of the specification"
 FT Region 50..250
 FT /note= "This region, TRASH protein #4, is specifically
 FT claimed in claim 28 of the specification"

US2002055474-A1.

09-MAY-2002.

27-JAN-1998; 98US-0014348.

27-JAN-1998; 98US-0014348.

XX

PA (BUSF/) BUSFIELD S J.

XX Busfield SJ;

XX WPI: 2002-526818/56.

DR N-PSDB; ABB6985.

PT New nucleic acid encoding a protein designated TRASH is a member of the
 PT tumor necrosis factor ligand superfamily of proteins and is useful to
 PT detect and treat TRASH-associated disorders including immune and
 PT inflammatory disorders -

XX Claim 28; Fig 1; 44pp; English.

CC The invention discloses an isolated nucleic acid encoding a novel tumour
 CC necrosis factor ligand (TNFL), referred to as TRASH (not defined) (or
 CC TANGO 118), protein. Members of the TNFL superfamily are involved in the
 CC activation of a large array of cellular genes and of multiple signal
 CC transduction pathways. Kinases and transcription factors. The nucleic
 CC acid and protein can be used in gene therapy, to identify compounds that
 CC modulates TRASH activity, raise antibodies and treat, or diagnose,
 CC disorders associated with aberrant TRASH activity or expression,
 CC particularly an immune response or inflammatory disorder, or a
 CC differential or developmental disorder. The sequence presented is the
 CC human tumour necrosis factor ligand (TNFL), TRASH protein #1.
 XX

SO Sequence 250 AA;

Query Match 100.0%; Score 1304; DB 23; Length 250;
 Best Local Similarity 100.0%; Pred. No. 4.1e-127;
 Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPASSPFLAPKGPNGGVPREPALSVALLMSGALGAVACAMALLTQOTELQSLRR 60
 DB 1 MPASSPFLAPKGPNGGVPREPALSVALLMSGALGAVACAMALLTQOTELQSLRR 60
 QY 61 EVSRLQGTGSPQNGEGYPMQSLPEQSSDALAEWNGERSRKRRAVLTOKOKHSHVHL 120
 DB 61 EVSRLQGTGSPQNGEGYPMQSLPEQSSDALAEWNGERSRKRRAVLTOKOKHSHVHL 120
 QY 121 VPINATSKDSDVTEVMQPALRRGRLQAGYGVRIQDAGVLLYSQVLFQDVTFTMGQ 180
 DB 121 VPINATSKDSDVTEVMQPALRRGRLQAGYGVRIQDAGVLLYSQVLFQDVTFTMGQ 180
 QY 181 VVSREGQROETLFRCLISMPSHDPRAVNSCYAGVFHLHOGDILSVIIPRAKLNLS 240
 DB 181 VVSREGQROETLFRCLISMPSHDPRAVNSCYAGVFHLHOGDILSVIIPRAKLNLS 240
 QY 241 HGTFLGFVKL 250
 DB 241 HGTFLGFVKL 250

RESULT 11
 ID ABB81486
 ABB81486 standard; Protein: 250 AA.

ABB81486;

02-SEP-2002 (first entry)

Human zTNF2 amino acid sequence SEQ ID NO:6.

XX Human; zTNF12; tumour necrosis factor receptor; cytosolic;
 KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;
 KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic;
 KW nephrotoxic; hypotensive; gene therapy; B lymphocyte; tumour;
 KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
 KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
 KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
 KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
 KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
 KW light chain neuropathy; hypertension; large vessel disease;

KW graft-versus host disease; graft rejection; Crohn's disease.
XX Homo sapiens.
OS
XX WO200238766-A2.
XX
XX 16-MAY-2002.
XX
XX 05-NOV-2001; 2001WO-US47018.
XX
XX 07-NOV-2000; 2000US-246449P.
XX 20-DEC-2000; 2000US-257131P.
XX 28-JUN-2001; 2001US-301715P.
XX 29-AUG-2001; 2001US-315656P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Gross JA, Xu W, Henne RM, Grant FJ;
XX WPI; 2002-508212/54.
XX
XX Novel isolated human tumor necrosis factor receptor polypeptide, termed
XX Znfir12, useful for treating autoimmune disorders, emphysema, end
XX stage renal failure or renal disease and lymphoma
XX
XX Disclosure; Page 135; 154pp; English.
XX
XX The present invention describes a human tumour necrosis factor receptor
XX designated znfir12 (I). (I) has cytostatic, immunosuppressive,
XX dermatological, antiinflammatory, neuroprotective, antidiabetic,
XX antirheumatic, antiarthritic, antiaesthetic, nephrotoxic and hypotensive
XX activities, and can be used in gene therapy. (I) can be used for
XX inhibiting, in a mammal, the activity of a ligand that binds znfir12
XX (e.g. ZTNF4), for treating disorders and diseases associated with B
XX lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
XX inhibiting the proliferation of tumour cells. (I) is useful for treating
XX autoimmune disorders such as systemic lupus erythematosus, myasthenia
XX gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
XX rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
XX or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
XX leukaemia, nephritis, and pyelonephritis, and for treating renal
XX neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
XX amyloidosis, hypertension, large vessel diseases, graft-versus host
XX disease, graft rejection and Crohn's disease. (I) is useful for
XX modulating the immune system, for regulating B cell responses and
XX development, for modulating development of other cells, antibody
XX production and cytokine production, and for modulating T and B cell
XX communication. The present sequence represents the human ZTNF2 protein
XX which is given in the exemplification of the present invention.
XX
XX Sequence 250 AA;
XX
XX Query Match 100.0%; Score 1304; DB 23; Length 250;
XX Best Local Similarity 100.0%; Pred. No. 4.1e-127;
XX Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 241 HGTFLEFVKL 250
|||||
RESULT 12
ABP47228
ID ABP47228 standard; Protein; 250 AA.
XX
XX ABP47228;
XX
XX 19-AUG-2002 (first entry)
XX
XX Human Blys binding scFv VH CDR3 SEQ ID 3239.
XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO200202641-A1.
XX
XX 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US19110.
XX
XX 16-JUN-2000; 2000US-212210P.
XX 17-OCT-2000; 2000US-240816P.
XX 16-MAR-2001; 2001US-276248P.
XX 21-MAR-2001; 2001US-277379P.
XX 25-MAY-2001; 2001US-293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114798/15.
XX
XX PT Antibodies against B lymphocyte Stimulating polypeptides, useful for
XX the diagnosis and treatment of cancers and immune disorders -
XX
XX Disclosure; Page 3147-3148; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
XX B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of Blys. The antibodies bind to Blys
XX and so may be used to detect and quantitate the presence of Blys in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of Blys. They may also be
XX administered to treat diseases associated with aberrant Blys expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method
XX of the invention.
XX
XX Sequence 250 AA;
XX
XX Query Match 100.0%; Score 1304; DB 23; Length 250;
XX Best Local Similarity 100.0%; Pred. No. 4.1e-127;
XX Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PS Claim 35; Fig 12A; 156pp; English.

XX This invention describes isolated Tumor Necrosis Factor (TNF) family
CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
CC their active fragments. APO4 is useful for diagnosing prostate cancer
CC by determining levels of APO4 in an individual. Prostate cancer can also
CC be treated using APO4 selective binding agents linked to a therapeutic
CC moiety. APO4 polypeptides are also useful for identifying selective
CC binding agents, useful in diagnosis/treatment of disease by binding of
CC agents to the polypeptide/active fragment which is extracellular, or
CC expressed on the cell surface. The binding is preferably performed in
CC vivo. APO4 polypeptides/active fragments are also useful for screening
CC for agonists and antagonists by binding and observing the change in APO4
CC activity. Effective pharmacological agents useful in diagnosis or
CC treatment of disease are also identified using APO4 polypeptides/active
CC fragments and APO4 signal transducer molecules that specifically interact
CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC activity. The method is performed in vivo or in vitro. APO polypeptides
CC are all useful as immunogens for preparing antibodies. APO4 is also
CC useful for diagnosis/treatment of developmental or gestational
CC abnormalities. APO8 was transfected to human breast carcinoma cell line
CC MCF-7, and induced apoptosis.

XX Sequence 250 AA;

XX

Query Match 99.6%; Score 1299; DB 20; Length 250;
Best Local Similarity 99.6%; Pred. No. 1.3e-126;
Matches 249; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPASSPFLAPKGPQNMGGVPRPALSVLWLSWGAALGAVACAMALLTQOTELQSLRR 60
DB 1 MPASSPFLAPKGPQNMGGVPRPALSVLWLSWGAALGAVACAMALLTQOTELQSLRR 60

QY 61 EVSRLOGTGSPQNGEGYPMQSLPEQSSDALFAWENGERSRKRRAVLTOKOKHSHVHL 120
DB 61 EVSRLOGTGSPQNGEGYPMQSLPEQSSDALFAWENGERSRKRRAVLTOKOKHSHVHL 120

QY 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYVRIDAGVYLLYSQVLFQDVTFTMGQ 180
DB 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYVRIDAGVYLLYSQVLFQDVTFTMGQ 180

QY 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCSAGVFHLHOGDILSVIIPARAKLNLS 240
DB 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCSAGVFHLHOGDILSVIIPARAKLNLS 240

QY 241 HGTFLGFPVKL 250
DB 241 HGTFLGFPVKL 250

RESULT 15
AAV79670
ID AAV79670 standard; Protein; 250 AA.

XX AAV79670;
AC
XX 29-AUG-2000 (first entry)
DT
XX
DE Human death receptor ligand-1 (DRL-1).
XX
XX DRL-1; human; death receptor ligand-1; tumor necrosis factor;
KM TNF-gamma; TNF-like ligand; TLL; immunostimulant; immunosuppressive;
KM T-cell response; transplant rejection; graft versus host disease;
KM apoptosis.
XX
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Domain 26..50
FT Domain /note= "putative transmembrane domain"
FT Domain 65..250
FT /note= "extracellular domain"

FT Modified-site 124
FT /note= "N-glycosylated"
XX
XX
XX NO200026244-A2.
XX
XX 11-MAY-2000.
PD
XX
XX 04-NOV-1999; 99MO-US25954.
PF
XX
XX 04-NOV-1998; 98US-0106976.
PR
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Lenardo MJ, Wang J, Jiang D;
DR WPI: 2000-365575/31.
DR N-PSDB; AAA27732.
XX
XX Novel nucleic acids encoding tumor necrosis factor family polypeptides
PT termed as Death Receptor Ligands useful for stimulating immune response
PT and inducing apoptosis comprising a specific nucleotide sequence -
XX
XX
PS Claim 6; Fig 1A; 80pp; English.

XX The present sequence is that of human death receptor ligand 1
CC (DRL-1), a novel member of the tumor necrosis factor (TNF) family,
CC also termed TNF-gamma or TNF-like ligand (TLL). The sequence was
CC deduced from cDNA (see AAA27732) isolated from a lymphoma cell line.
CC DRL-1 is expressed as a 1.8 kb transcript in heart, placenta, lung,
CC kidney and pancreas. In the lymphoid tissue, it is expressed in
CC the peripheral lymphoid organs but not in the thymus or foetal
CC liver. The invention provides human and murine DRL polypeptides,
CC nucleic acids and antibodies. DRL-1 polypeptides are used in
CC claimed methods of stimulating an immune response and of inducing
CC apoptosis in a population of T-cells. Antibodies to DRL-1 are
CC used in claimed methods of suppressing an immune response,
CC inhibiting a T-cell response associated with transplant rejection
CC or graft versus host disease, inhibiting apoptosis in a population
CC of T cells, and of stimulating the membrane-bound form of DRL-1.

XX

XX Sequence 250 AA;

Query Match 99.6%; Score 1299; DB 21; Length 250;
Best Local Similarity 99.6%; Pred. No. 1.3e-126;
Matches 249; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPASSPFLAPKGPQNMGGVPRPALSVLWLSWGAALGAVACAMALLTQOTELQSLRR 60
DB 1 MPASSPFLAPKGPQNMGGVPRPALSVLWLSWGAALGAVACAMALLTQOTELQSLRR 60

QY 61 EVSRLOGTGSPQNGEGYPMQSLPEQSSDALFAWENGERSRKRRAVLTOKOKHSHVHL 120
DB 61 EVSRLOGTGSPQNGEGYPMQSLPEQSSDALFAWENGERSRKRRAVLTOKOKHSHVHL 120

QY 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYVRIDAGVYLLYSQVLFQDVTFTMGQ 180
DB 121 VPINATSKDSDVTEVMQPALRRGRGLQAGYVRIDAGVYLLYSQVLFQDVTFTMGQ 180

QY 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCSAGVFHLHOGDILSVIIPARAKLNLS 240
DB 181 VVSREGQGRQETLFRICIRSMPSHPDRAYNSCSAGVFHLHOGDILSVIIPARAKLNLS 240

QY 241 HGTFLGFPVKL 250
DB 241 HGTFLGFPVKL 250

Search completed: March 26, 2003, 07:34:01
Job time : 77 secs